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- **NILSSON I M ET AL: "Induction of split tolerance and clinical cure in high-responding hemophiliacs with factor IX antibodies" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 83, no. 23, 1986, pages 9169-9173, XP002164050 1986 ISSN: 0027-8424**
- **BAJAJ S P ET AL: "A monoclonal antibody to factor IX that inhibits the factor VIII:Ca potentiation of factor X activation" JOURNAL OF BIOLOGICAL CHEMISTRY, THE AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, INC., US, vol. 260, no. 21, 25 September 1985 (1985-09-25), pages 11574-11576, 11578-11580, XP002922137 ISSN: 0021-9258**

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Description

[0001] Blood clots (thrombi) are formed by a series of zymogen activations referred to as the coagulation cascade. In the course of this enzymatic cascade, the activated form of each of such zymogens (referred to as factors) catalyzes the activation of the next one. Thrombi are deposits of blood components on the surface of a blood vessel wall and mainly consist of aggregated blood platelets and insoluble, cross-linked fibrin. Fibrin formation is effected by means of thrombin by limited proteolysis of fibrinogen. Thrombin is the final product of the coagulation cascade, (K.G. Mann, Blood, 1990, Vol. 76, pp.1-16).

[0002] Activation of factor X by the complex of activated factor IX (FIXa) and activated factor VIII (FVIIIa) is a key step in coagulation. The absence of the components of this complex or a disturbance of their function is associated with the blood coagulation disorder called hemophilia (J.E. Sadler & E.W. Davie: Hemophilia A, Hemophilia B and von Willebrand's disease, in G. Stamatoyannopoulos et al. (Eds.): The molecular basis of blood diseases. W.B. Saunders Co., Philadelphia, 1987, pp. 576-602). Hemophilia A denotes a (functional) absence of factor VIII activity, while Hemophilia B is characterized by the absence of factor IX activity. At present, treatment of Hemophilia A is effected via a substitution therapy by administering factor VIII concentrates. However, approximately 20-30% of Hemophilia A patients develop factor VIII inhibitors (i.e. antibodies against factor VIII), whereby the effect of administered factor VIII preparations is inhibited. Treatment of factor VIII inhibitor patients is very difficult and involves risks, and so far there exist only a limited number of treatments for these patients.

[0003] In the case of patients having a low FVIII inhibitor level, it is possible, though expensive, to administer high doses of factor VIII to such patients and thus to neutralize the antibodies against factor VIII. The amount of factor VIII beyond that needed to neutralize the inhibitor antibodies then has hemostatic action. In many cases, desensitization can be effected, whereupon it is then possible again to apply standard factor VIII treatments. Such high dose factor VIII treatments require, however, large amounts of factor VIII, are time-consuming and may involve severe anaphylactic side reactions. Alternatively, the treatment may be carried out with porcine factor VIII molecules.

[0004] A further high-cost method involves removing factor VIII inhibitors through extra corporeal immunoadsorption on lectins which bind to immunoglobulins (protein A, protein G) or to immobilized factor VIII. Since the patient must be connected to an apheresis machine during this treatment, the treatment also constitutes a great burden on the patient. It is also not possible to treat an acute hemorrhage in this way.

[0005] At present, the therapy of choice is to administer activated prothrombin complex concentrates (APCC), such as FEIBA® and AUTOPLEX®, which are suitable for the treatment of acute hemorrhages even in patients having a high inhibitor titer (DE 31 27 318).

[0006] In the intravascular system of blood coagulation, the last step is the activation of factor X. This reaction is stimulated by the binding of factor VIIIa to factor IXa and the formation of a "tenase"-complex consisting of the factors IXa, VIIIa, X and phospholipid. Without the binding of FVIIIa, FIXa exhibits no or only a very slight enzymatic activity relative to FX.

Over the last several years, a number of possible binding sites for factor VIIIa to factor IXa have been characterized, and it has been shown that antibodies or peptides which bind to these regions inhibit the activity of FIXa (Fay et al., J. Biol. Chem., 1994, Vol.269, pp.20522-20527, Lenting et al., J. Biol. Chem., 1996, Vol. 271, pp. 1935-1940, Jorquera et al., Circulation, 1992, Vol. 86, Abstract 2725). The inhibition of coagulation factors, such as factor IX, has also been achieved through the use of monoclonal antibodies with the aim of preventing thrombosis formation (WO 97/26010). The opposite effect, i.e. an increase in the factor IXa mediated activation of factor X, has been described by Liles D.K. et al., (Blood, 1997, Vol. 90, suppl. 1, 2054) through the binding of a factor VIII peptide (amino acids 698-712) to factor IX. Yet, this effect only occurs in the absence of factor VIIIa, while in the presence of factor VIIIa the factor IXa/factor VIIIa-mediated cleavage of factor X is inhibited by this peptide.

[0007] Further, WO 86/06101 describes a series of proteins which exhibit procoagulant properties.

[0008] With a view to the possible risks and side effects which may occur in the treatment of hemophilia patients, there is a need for a therapy which allows for the effective treatment of FVIII inhibitor patients. Therefore, it is an object of the present invention to provide a preparation for the treatment of blood coagulation disorders which has particular advantages for factor VIII inhibitor patients.

According to the present invention, this object is achieved through the use of antibodies against factor IX/factor IXa which have factor VIIIa-cofactor activity and lead to an increase in the procoagulant activity of factor IXa. Surprisingly, the action of these inventive factor IX/factor IXa-activating antibodies is not negatively affected by the presence of inhibitors, such as inhibitors against factor VIII/factor VIIIa, but instead the procoagulant activity of factor IXa in this case also is increased.

[0009] A further advantage of this invention is that the administration of the preparation according to the invention allows for rapid blood coagulation even in the absence of factor VIII or factor VIIIa, even in the case of FVIII inhibitor patients. Surprisingly, these agents are also effective in the presence of factor VIIIa.

[0010] The antibodies according to the present invention thus have a FVIII-cofactor-like activity which, in a FVIII assay

(e.g. a COATEST® assay or Immunochrom test) after 2 hours of incubation exhibits a ratio of background (basic noise) to measured value of at least 3. Calculation of this ratio may, e.g., be effected according to the following scheme:

Antibody measurement (OD 405) – blank value from reagent > 3

Mouse-IgG-measurement (OD 405) – blank value from reagent

after two hours of incubation.

[0011] The antibodies according to the invention preferably have an in vivo half life of at least 5 days, more preferably at least 10 days, though it is more preferred to have a half life of at least 20 days.

[0012] A further aspect of this invention is a preparation comprising antibodies against factor IX/factor IXa and a pharmaceutically acceptable carrier substance. Furthermore, the preparation according to the invention may additionally comprise factor IX and/or factor IXa.

[0013] A further aspect of the invention is the use of the antibodies to increase the amidolytic activity of factor IXa.

Fig. 1 shows the results of a screening of supernatants from hybridoma cell cultures for FVIII-like activity. Pre-selected clones from fusion experiments, #193, #195 and #196, were tested in a chromogenic assay.

Fig. 2 shows the results of screening for IgG-mediated factor VIII-like activity in supernatants of a hybridoma cell culture of a master plate.

Fig. 3 shows the subcloning of clone 193/C0, namely the results of the first cloning round.

Fig. 4 shows a comparison of the chromogenic FVIII-like activity and factor IX-ELISA-reactivity of hybridoma cultures derived from the starting clone 193/C0.

Fig. 5 shows the results of the measurement of the chromogenic activity of some master clones and subclones.

Fig. 6A shows the FVIII-like activity of the anti-FIX/FIXa-antibodies 193/AD3 and 196/AF2 compared to human FVIII, TBS buffer and cell culture medium. After a lag phase, both antibodies gave rise to chromogenic substrate cleavage, as judged by the increasing optical density.

Fig. 6B shows a comparison of the chromogenic activity of factor VIII, 196/AF1, 198/AC1/1 and mouse-IgG.

Fig. 7A shows a comparison of the kinetics of Factor Xa generation by Factor VIII and 196/AF2 with and without the addition of a Factor Xa specific inhibitor.

Fig. 7B shows a comparison of the kinetics of the Factor Xa generation by Factor VIII, mouse-IgG and anti-factor IX/IXa-antibody 198/AM1 with and without the addition of a factor Xa-specific inhibitor, Pefabloc Xa®.

Fig. 8A shows a measurement of the dependence of the factor VIII-like activity of purified anti-factor IX/IXa-antibody 198/AC1/1 in the presence and absence of phospholipids, FIXa/FX and calcium ions.

Fig. 8B shows a measurement of the dependence of FXa generation by anti-FIXa-antibody 196/AF1 in the presence of phospholipids, Ca²⁺ in FIXa/FX.

Fig. 8C shows the generation of FXa by unspecific mouse IgG antibody.

Fig. 9 is a graphical representation of the coagulation times of Factor VIII-deficient plasma in an APTT assay by using various concentrations of anti-factor IX/IXa-antibody 193/AD3.

Fig. 10A shows that in the presence of Factor IXa, antibody 193/AD3 leads to a reduction in the coagulation time of factor VIII-deficient plasma.

Fig. 10B shows a dose-dependent reduction of the clotting time by antibody 193/AD3 in the presence of factor IXa and factor VIII-inhibitors.

Fig. 11 shows the chromogenic activity of antibodies 198/A1, 198/B1 and 198/AP1 in the presence and absence of human FIXaβ.

Fig. 12 shows the primer sequences for the amplification of the genes of the variable heavy chain of mouse antibody.

Fig. 13 shows the primer sequences for the amplification of the genes of the variable light (kappa) chain of the mouse antibody.

Fig. 14 shows the DNA and derived protein sequence of the scFv from hybridoma cell line 193/AD3 (SEQ.ID.NOs. 81 and 82).

Fig. 15 shows the DNA and derived protein sequence of the scFv from hybridoma cell line 193/K2 (SEQ.ID.NOs. 83 and 84).

Fig. 16 shows the DNA and derived protein sequence of the scFv from hybridoma cell line 198/AB2 (subclone of 198/B1) (SEQ.ID.NOs. 85 and 86).

Fig. 17 shows the DNA and deduced protein sequence of scFv derived from the cell line 198/A1 (SEQ.ID.NOs. 87 and 88).

Fig. 18 demonstrates the chromogenic FVIII-like activity of peptide A1/3 in the presence of 2.9nM human FIXa. The

scrambled version of peptide A1/3, peptide A1/5 does not give rise to any FXa generation.

Fig. 19 demonstrates the dependence of the chromogenic FVIII-like activity of peptide A1/3 on the presence of human FIXa. In the absence of human FIXa, peptide A1/3 does not give rise to any FXa generation. The buffer control, plain imidazole buffer is designated IZ.

Fig. 20 shows that the chirality of Arg-residues does not play a significant role for the chromogenic activity of peptides A1/3-rd and A1/3-Rd-srmb.

Fig. 21 shows that the addition of 2.4 μ M peptide B1/7 to the reaction mixture led to a measureable generation of Fxa.

Fig. 22 shows that the addition of a FX-specific inhibitor results in a significant reduction in the reaction. If there was no FIXa and FX is added to the reaction mixture, no FXa was synthesized.

Fig. 23 shows vector pBax-IgG1.

Fig. 24 shows the increase of the amidolytic activity of FIXa in the presence of antibody 198/B1 (Fig. 24A) and IgM antibody 198/AF1 (Fig. 24B).

Fig. 25 demonstrates the chromogenic FVIII-like activity of the antibody 198/A1 Fab fragment in the presence of 2.3nM human FIXa. As a positive control the intact antibody 198/A1 was used as well as 7.5pM FVIII. The buffer control (IZ) was used as a negative control.

Fig. 26 shows the nucleotide and amino acid sequence of the 198AB2 scFv-alkaline phosphatase fusion protein (ORF of the expression vector pDAP2-198AB2#100, (SEQ.ID.NOs. 89 and 90).

The genes for the VL and the VH domains of antibody 198/AB2 (198/AB2 is an identical subclone of 198/B1) were derived from the corresponding hybridoma cells as described in example 10. The PCR product of the VH-gene was digested SfiI - Ascl and the PCR-product of the VL-gene was digested Ascl and NotI. VH and VL genes were linked via the Ascl site and inserted into SfiI - NotI digested vector pDAP2 (Kerschbaumer R.J. et al, Immunotechnology 2, 145-150, 1996; GeneBank accession No.:U35316). PelB leader: leader sequence of *Erwinia carotovora* Pectate Lyase B, His tag, Histidine tag for metal ion chromatography.

Fig. 27 demonstrates the chromogenic FVIII-like activity of two antibody 198/B1 (subclone AB2) scFv fragment-alkaline phosphatase fusion proteins (198AB2#1 and 198AB2#100) in the presence of 2.3nM human FIXa. As a positive control 7.5pM FVIII was used.

Fig. 28 shows the amino acid and nucleotide sequence of pZip198AB2#102 (SEQ.ID.NOs. 91 and 92).

Fig. 29 shows the nucleotide and amino acid sequence of the mAB#8860 scFv-alkaline phosphatase fusion protein (vector pDAP2-8860scFv#11, (SEQ.ID.NOs. 93 and 94). The genes for the VL and the VH domains of antibody #8860 were derived from the corresponding hybridoma cells as described in example 10. The PCR product of the VH-gene was digested SfiI - Ascl and the PCR-product of the VL-gene was digested Ascl and NotI. VH and VL genes were linked via the Ascl site and inserted into SfiI - NotI digested vector pDAP2 (Kerschbaumer R.J. et al, Immunotechnology 2, 145-150, 1996; GeneBank accession No.:U35316).

Fig. 30 shows the nucleotide and amino acid sequence of the mAB #8860 scFv-leucine zipper fusion protein (mini-antibody; vector p8860-Zip#1.2, (SEQ.ID.NOs. 95 and 96). The gene of the scFv fragment was derived from mAB #8860 and was swapped from vector pDAP2-8860scFv#11 into SfiI-NotI digested plasmid pZip1 (Kerschbaumer R.J. et al., Analytical Biochemistry 249, 219-227, 1997; GeneBank accession No.: U94951)

Fig. 31 demonstrates the chromogenic FVIII-like activity of the 198/B1 (subclone AB2) miniantibody 198AB-Zip#102 in the presence of 2.3nM human FIXa. As a positive control 4.8pM FVIII was used whereas a unrelated miniantibody (8860-Zip#1.2) and plain reaction buffer (IZ) served as negative controls.

Fig. 32 shows a schematic representation of the plasmid pMycHis6.

Fig. 33 shows the nucleotide and amino acid sequence of the part of the plasmid pMycHis6 differing from vector pCOCK (SEQ.ID.NOs. 97 and 98). Vector pMycHis6 was constructed by cleaving vector pCOCK (Engelhardt et al., 1994, Biotechniques, 17:44-46) with NotI and EcoRI and insertion of the oligonucleotides: mychis6-co: 5'ggcgcgaacaaaaactcatctcagaagaggatct gaatggggcgccacatccatccatcactaataag 3' (SEQ ID.No. 79) and mychis-ic: , 5'aattcttattagtgatggtgatggtgatgtgccgccccattcagatcctctct gagatgagttttgttctgc (SEQ.ID.No. 80).

Fig. 34 shows the nucleotide and amino acid sequence of 198AB2 scFv (linked to the c-myc-tag and the His6- tag): ORF of the expression vector pMycHis6-198AB2#102. Vector pMycHis6 was constructed by cleaving vector pCOCK (Engelhardt O. et al, BioTechniques 17, 44-46, 1994) NotI - EcoRI and inserting the following annealed oligonucleotides:

(5' -GGCCGCAGAACAAAACTCATCTCAGAAGAGGATCTGAATGGG

GCGGCACATCACCATCACCATCACTAATAAG - 3' (SEQ.ID.No. 103)

and

5'- TTATTAGTGATGGTGATGGT GATGTGCCGCCCCATTGAGATCCTCTTCTGAGATGAGTTTTTGTCTGC-3'

(SEQ.ID.NO. 104)). The resultant vector, named pMycHis6, was cleaved SfiI - NotI and the gene of scFv 198AB2 was swapped into this vector from vector pDAP2-198AB2#100.

Fig. 35 shows the nucleotide and amino acid sequence of the mAb #8860 scFv linked to the c-myc-tag and the His6- tag (vector p8860-M/H#4c, SEQ.ID.NO.s. 101 and 102). Plasmid pMycHis6 was cleaved with SfiI and NotI and the DNA sequence coding for the scFv 8860#11 protein was inserted from pDAP2-8860scFv#11 (see Fig.29) yielding plasmid p8860-M/H#4c.

Fig. 36 demonstrates the chromogenic FVIII-like activity of the 198/B1 (subclone AB2) scFv fragment (MycHis-198AB2#102) in the presence of 2.3nM human FIXa. As a positive control 4.8pM FVIII was used whereas a unrelated scFv (8860-M/H#4c) and plain reaction buffer (IZ) served as negative controls.

Antibodies

[0014] The present invention also comprises the nucleic acids encoding the inventive antibodies expression vectors, hybridoma cell lines, and methods for producing the same.

[0015] Antibodies are immunoglobulin molecules having a specific amino acid sequence which only bind to antigens that induce their synthesis (or its immunogen, respectively) or to antigens (or immunogens) which are very similar to the former. Each immunoglobulin molecule consists of two types of polypeptide chains. Each molecule consists of large, identical heavy chains (H chains) and two light, also identical chains (L chains). The polypeptides are connected by disulfide bridges and non-covalent bonds. In vivo, the heavy and light chains are formed on different ribosomes, assembled in the cell, and secreted as intact immunoglobulins (Roitt I. et al., in: Immunology, second ed., 1989).

[0016] The inventive antibodies and organic compounds derived there from comprise human and animal monoclonal antibodies or fragments thereof, single chain antibodies and fragments thereof and miniantibodies, bispecific antibodies, diabodies, triabodies, or di-, oligo- or multimers thereof. Also included are peptidomimetics or peptides derived from the antibodies according to the invention, e.g. they comprise one or several CDR regions, preferably the CDR3 region.

[0017] Further included are human monoclonal antibodies and peptide sequences which, based on a structure activity connection, are produced through an artificial modeling process (Greer J. et al., J. Med. Chem., 1994, Vol. 37, pp. 1035-1054).

[0018] The term factor IX/IXa activating antibodies may also include proteins produced by expression of an altered, immunoglobulin-encoding region in a host cell, e.g. "technically modified antibodies" such as synthetic antibodies, chimeric or humanized antibodies, or mixtures thereof, or antibody fragments which partially or completely lack the constant region, e.g. Fv, Fab, Fab' or F(ab)'₂ etc. In these technically modified antibodies, e.g., a part or parts of the light and/or heavy chain may be substituted. Such molecules may, e.g., comprise antibodies consisting of a humanized heavy chain and an unmodified light chain (or chimeric light chain), or vice versa. The terms Fv, Fc, Fd, Fab, Fab' or F(ab)₂ are used as described in the prior art (Harlow E. and Lane D., in "Antibodies, A Laboratory Manual", Cold Spring Harbor Laboratory, 1988).

[0019] The present invention also comprises the use of Fab fragments or F(ab)₂ fragments which are derived from monoclonal antibodies (mAb), which are directed against factor IX/factor IXa and cause an increase of the procoagulant activity of factor IXa. Preferably, the heterologous framework regions and constant regions are selected from the human immunoglobulin classes and isotypes, such as IgG (subtypes 1 to 4), IgM, IgA and IgE. In the course of the immune response, a class switch of the immunoglobulins may occur, e.g. a switch from IgM to IgG; therein, the constant regions are exchanged, e.g. from μ to γ . A class switch may also be caused in a directed manner by means of genetic engineering methods ("directed class switch recombination"), as is known from the prior art (Esser C. and Radbruch A., Annu. Rev. Immunol., 1990, Vol. 8, pp. 717-735). However, the antibodies according to the present invention need not comprise exclusively human sequences of the immunoglobulin proteins.

[0020] In one particular embodiment, a humanized antibody comprises complement determining regions (CDRs) from murine monoclonal antibodies which are inserted in the framework regions of selected human antibody sequences. However, human CDR regions can also be used. Preferably, the variable regions in the human light and heavy chains are technically altered by one or more CDR exchanges. It is also possible to use all six CDRs or varying combinations of less than six CDRs.

[0021] The humanized antibody according to the present invention preferably has the structure of a human antibody or of a fragment thereof and comprises the combination of characteristics necessary for a therapeutic application, e.g., the treatment of coagulation disorders in patients, preferably factor VIII inhibitor patients.

[0022] A chimeric antibody differs from a humanized antibody in that it comprises the entire variable regions including the framework regions of the heavy and light chains of non-human origin in combination with the constant regions of both chains from human immunoglobulin. A chimeric antibody consisting of murine and human sequences may, for example, be produced. According to the present invention, the antibodies may also be single chain antibodies or mini-antibodies (scFv fragments, which, e.g., are linked to proline-rich sequences and oligomerisation domains, e.g. Pluckthun A. and Pack P., Immunotechnology, 1997, Vol. 3, pp. 83-105) or single chain Fv (sFv) which incorporate the entire

antibody binding region in one single polypeptide chain. For instance, single chain antibodies may be formed by linking the V-genes to an oligonucleotide which has been constructed as a linker sequence and connects the C terminus of the first V region with the N terminus of the second V region, e.g. in the arrangement V_H-Linker-V_L or V_L-Linker-V_H; both, V_H and V_L thus may represent the N-terminal domain (Huston JS et al., *Int. Rev. Immunol.*, 1993, Vol. 10, pp. 195-217; Raag R. and Whitlow M., *FASEB J.*, 1995, Vol. 9, pp. 73-80). The protein which can be used as linker sequence may, e.g., have a length of up to 150 Å, preferably up to 80 Å, and more preferably up to 40 Å. Linker sequences containing glycine and serine are particularly preferred for their flexibility, or glutamine and lysine, respectively, for their solubility. The choice of the amino acid is effected according to the criteria of immunogenicity and stability, also depending on whether or not these single chain antibodies are to be suitable for physiological or industrial applications (e.g. immunoaffinity chromatography). The single chain antibodies may also be present as aggregates, e.g. as trimers, oligomers or multimers. The linker sequence may, however, also be missing, and the connection of the V_H and V_L chains may occur directly.

[0023] Bispecific antibodies are macromolecular, heterobifunctional cross-linkers having two different binding specificities within one single molecule. In this group belong, e.g., bispecific (bs) IgGs, bs IgM-IgAs, bs IgA-dimers, bs (Fab')₂, bs(scFv)₂, diabodies, and bs bis Fab Fc (Cao Y. and Suresh M.R., *Bioconjugate Chem.*, 1998, Vol. 9, pp. 635-644).

[0024] By peptidomimetics, protein components of low molecular weight are understood which imitate the structure of a natural peptide component, or of templates which induce a specific structure formation in an adjacent peptide sequence (Kemp DS, *Trends Biotechnol.*, 1990, pp. 249-255). The peptidomimetics may, e.g., be derived from the CDR3 domains. Methodical mutational analysis of a given peptide sequence, i.e. by alanine or glutamic acid scanning mutational analysis, allows for the identification of peptide residues critical for procoagulant activity. Another possibility to improve the activity of a certain peptide sequence is the use of peptide libraries combined with high throughput screening.

[0025] The term antibodies may also comprise agents which have been obtained by analysis of data relating to structure-activity relationships. These compounds may also be used as peptidomimetics (Grassy G. et al., *Nature Biotechnol.*, 1998, Vol. 16, pp. 748-752; Greer J. et al., *J. Med. Chem.*, 1994, Vol. 37, pp. 1035-1054).

[0026] Examples of hybridoma cells expressing the antibodies according to the invention were deposited on 9 September 1999 under the numbers 99090924 (#198/A1), 99090925 (#198/B1) and 99090926 (#198/BB1) and on December 16, 1999 under the numbers 99121614 (#193/A0), 99121615 (#196/C4), 99121616 (#198/D1), 99121617 (198/T2), 99121618 (#198/G2), 99121619 (#198/AC1) and 99121620 (#198/U2) according to the Budapest Treaty.

Methods of Production:

[0027] The antibodies of the present invention can be prepared by methods known from the prior art, e.g. by conventional hybridoma techniques, or by means of phage display gene libraries, immunoglobulin chain shuffling or humanizing techniques (Harlow E. and Lane D., in: *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988). The production of the inventive antibodies and antibody derivatives may, for instance, be made by conventional hybridoma techniques (*Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, Eds. Harlow and Lane, pp. 148-242). According to the present invention, non-human species may be employed therefor, such as cattle, pigs, monkeys, chickens and rodents (mice, rats). Normal, immunocompetent Balb/c mice or FIX-deficient mice may, e.g., be used (factor IX-deficient mice may be obtained from Dr. Darrel Stafford from the University of North Carolina, Chapel Hill). Immunization may, e.g., be effected with factor IX, factor IXα or completely activated factor IXαβ, or with fragments thereof.

[0028] The hybridomas are selected with a view to the fact that the antibodies in the supernatants of the hybridoma cells bind to factor IX/factor IXα and cause an increase of the procoagulant activity of factor IXα. The increase in the procoagulant activity may, e.g., be proven by assaying methods as known from the prior art for the measurement of factor VIII-like activity, e.g. chromogenic assays.

[0029] Alternatively, the antibodies of the invention may also be produced by recombinant production methods. In doing so, the DNA sequence of the antibodies according to the invention can be determined by known techniques, and the entire antibody DNA or parts thereof can be expressed in suitable systems. Recombinant production methods can be used, such as those involving phage display, synthetic and natural libraries, expression of the antibody proteins in known expression systems, or expression in transgenic animals (Jones et al., *Nature*, 1986, Vol. 321, pp.522-525; *Phage Display of Peptides and Proteins, A Laboratory Manual*, 1996, Eds. Kay et al., pp. 127-139; US 4,873,316; Vaughan T.J. et al., *Nature Biotechnology*, 1998, pp. 535-539; Persic L. et al., *Gene*, 1997, pp. 9-18; Ames R.S. et al., *J. Immunol. Methods*, 1995, pp. 177-186).

[0030] The expression of recombinantly produced antibodies may be effected by means of conventional expression vectors, such as bacterial vectors, such as pBr322 and its derivatives, pSKF or eukaryotic vectors, such as pMSG and SV40 vectors. Those sequences which encode the antibody may be provided with regulatory sequences which regulate the replication, expression and secretion from the host cell. These regulatory sequences comprise promoters, e.g. CMV or SV40, and signal sequences.

[0031] The expression vectors may also comprise selection and amplification markers, such as the dihydrofolate reductase gene (DHFR), hygromycin-B- phosphotransferase, thymidine-kinase etc.

[0032] The components of the vectors used, such as selection markers, replicons, enhancers etc., may either be commercially obtained or prepared by means of conventional methods. The vectors may be constructed for the expression in various cell cultures, e.g. for mammalian cells such as CHO, COS, fibroblasts, insect cells, yeast or bacteria, such as E. coli. Preferably, those cells are used which allow for an optimal glycosylation of the expressed protein. Particularly preferred is the vector pBax (cf. Fig. 17) which is expressed in CHO cells or in SK-Hep.

The production of Fab fragments or F(ab)₂ fragments may be effected according to methods known from the prior art, e.g. by cleaving a mAb with proteolytic enzymes, such as papain and/or pepsin, or by recombinant methods. These Fab and F(ab)₂ fragments may also be prepared by means of a phage display gene library (Winter et al., 1994, Ann. Rev. Immunol., 12:433-455).

The purification of the inventive antibodies may also be carried out by methods described in the prior art, e.g., by ammonium sulfate precipitation, affinity purification (protein G-Sepharose), ion exchange chromatography, or gel chromatography. The following methods may be used as the test methods to show that the antibodies of the present invention bind to factor IX/factor IXa, increase the procoagulant activity of factor IXa or have factor VIII-like activity.: the one step coagulation test (Mikaelsson and Oswaldson, Scand. J. Haematol., Suppl., 33, pp. 79-86, 1984) or the chromogenic tests, such as COATEST VIII:C® (Chromogenix) or Immunochrom (IMMUNO). In principle, all the methods used for determining factor VIII activity may be used. As the control blank value for the measurements, e.g., unspecific mouse-IgG antibody may be used.

[0033] The present antibodies are suitable for therapeutic use in the treatment of coagulation disorders, e.g. in the case of hemophilia A, for factor VIII inhibitor patients etc. Administration may be effected by any method suitable to effectively administer the therapeutic agent to the patient, e.g. by oral, subcutaneous, intramuscular, intravenous or intranasal administration.

[0034] Therapeutic agents according to the invention may be produced as preparations which comprise a sufficient amount of antibodies as the active agent in a pharmaceutically acceptable carrier substance. These agents may be present either in liquid or in powdered form. Moreover, the preparations according to the invention may also comprise mixtures of different antibodies, the derivatives thereof and/or organic compounds derived therefrom, as well as mixtures consisting of antibodies and factor IX and/or factor IXa. Factor IXa may be present as factor IXa α and/or factor IXa β . An example of an aqueous carrier substance is, e.g., saline. The solutions are sterile, sterilisation being effected by conventional methods.

[0035] The antibodies according to the invention may be present in lyophilized form for storage and be suspended in a suitable solvent before administration. This method has proven generally advantageous for conventional immunoglobulins, and known lyophilisation and reconstitution methods may be applied in this case.

[0036] Moreover, the antibodies according to the invention may also be used for industrial applications, e.g. for the purification of factor IX/factor IXa by means of affinity chromatography, or as a component of detection methods (e.g. ELISA assays), or as an agent for identification of and interaction with functional domains of a target protein.

[0037] The present invention will be described in more detail by way of the following examples and drawing figures.

Examples

Example 1: Immunization of immunocompetent mice and generation of anti-FIX/IXa antibody secreting hybridoma cells

[0038] Groups of 1-3 normal immunocompetent 5-8 week old Balb/c mice were immunized with 100 μ g antigen (100 μ l doses) via the intraperitoneal (i.p.) route. In a typical experiment, mice were inoculated with either recombinant human coagulation factor (F) IX (Benefix™), human activated FIXa α (Enzyme Research Laboratories, Lot: FIXa α 1190L) or human FIXa β (Enzyme Research Laboratories, Lot: HFIXAa β 1332 AL,) adjuvanted with Al(OH)₃ or KFA.

[0039] Individual mice were boosted at various times with 100 μ g antigen (100 μ l doses, i.p) and sacrificed two days later. Spleen cells were removed and fused to P3 X63-Ag8 6.5.3 myeloma cells essentially as described by Lane et al., 1985 (J. Immunol. Methods, Vol. 81, pp. 223-228). Each fusion experiment was individually numbered, i.e. #193, 195, 196 or 198.

[0040] Hybridoma cells were grown in 96 well plates on a macrophage feeder layer (app. 10⁵ cells/ml) and selected in HAT-medium (RPMI-1640 medium supplemented with antibiotics, 10% FCS, Na-pyruvate, L-glutamine, 2-mercaptoethanol and HAT (HAT 100x: 1.0x10⁻²M hypoxanthine in H₂O (136.1 mg/100ml H₂O), 4.0x10⁻⁵M aminopterin in H₂O (1.76 mg/100ml H₂O) and 1.6x10⁻³M thymidine in H₂O (38.7 mg/100ml H₂O). Medium was first changed after 6 days and thereafter twice a week. After 2-3 weeks HAT-medium was changed to HT-medium (RPMI-1640 supplemented with antibiotics, 10%FCS, Na-pyruvate, L-glutamine, 2-mercaptoethanol and HT) and later on (after additional 1-2 weeks) to normal growth medium (RPMI-1640 medium supplemented with 10%FCS, Na-pyruvate, L-glutamine and 2-mercap-

toethanol) (see: HYBRIDOMA TECHNIQUES, EMBO, SKMB Course 1980, Basel).

[0041] In another set of experiments FIX deficient C57B16 mice (Lin et al., 1997, Blood, 90:3962) were used for immunization and subsequent hybridoma production. Since FIX knockout (k.o.) mice do not express endogenous FIX, the anti (a)-FIX antibody spectrum achievable is supposed to be different compared to normal Balb/c mice (due to lack of tolerance)

Example 2: Assaying for FVIII-like activity in supernatants of anti-FIX/FIXa antibody secreting hybridoma cells

[0042] In order to assay the FVIII-like activity of anti-FIXa antibodies secreted by hybridoma cells, the commercially available test-kit COATEST VIII:C/4® (Chromogenix) was employed. The assay was done essentially as described by the manufacturer with the following modifications:

[0043] To allow high throughput screening, the assay was downscaled to microtiter plate format. Briefly, 25µl aliquots of hybridoma supernatants were transferred to microtiter plate (Costar, #3598) wells and warmed to 37 °C. Chromogenic substrate (S-2222), synthetic thrombin inhibitor (I-2581), factor (F) IXa and FX were reconstituted in sterile water and FIXa/FX was mixed with phospholipids according to the supplier's protocol. Per reaction, 50µl of the phospholipid/FIXa/FX solution were combined with 25µl CaCl₂ (25mM) and 50µl of the substrate/inhibitor cocktail. To start the reaction, 125µl of the premix were added to the hybridoma supernatant in the microtiter plates and incubated at 37 °C. Absorbency at 405nm and 490nm of the samples was read at various times (30min to 12h) against a reagent blank (MLW, cell culture medium instead of hybridoma supernatant) in a Labsystems iEMS Reader MF™ microtiter plate reader. FVIII-like activity of the samples was calculated by comparing the absorbency of the samples against the absorbency of a diluted FVIII reference standard (IMMUNO AG # 5T4AR00) using GENESIS™ software.

[0044] The results of a screening for FVIII-like activity in hybridoma cell culture supernatants are shown in Fig. 1. Pre-selected clones derived from fusion experiments #193, #195 and #196 (see above) were examined in a chromogenic FVIII assay as described. Clones 193/M1, 193/N1 and 193/P1 are subclones derived from the master clone 193/C0 (see below). Master clone 195/10 was derived from fusion experiment #195 and clones 196/A0, 196/B0 and 196/C0 were derived from fusion experiment #196. In a typical screening experiment, approximately 1000 clones (in 96 wells) from a single fusion experiment were pre-screened for FVIII-like activity. Subsequently, selected clones were grown on a larger scale (3-5 ml supernatant) and re-analyzed in a chromogenic assay. As a negative control cell culture medium was assayed on each plate (MLW).

[0045] Wells either exhibiting high FVIII-like activity or substantial FVIII-like activity were subjected to subcloning procedures. The selection and subcloning process is exemplified for the screening and subcloning of an IgG producing cell line (i.e. 193/C0) but has been done exactly the same way for an IgM (i.e. 196/C0, see below, Fig. 5) producing clone.

[0046] The selection process was done by initially plating all hybridoma cell clones derived from a single fusion experiment on ten 96 well plates thereby creating the so called "master plates". Singular positions (wells) on a master plate usually contained more than one hybridoma cell clone (usually 3 to 15 different clones). Subsequently, the antibody secreted by only several thousand cells was tested. These cells grew under conditions suboptimal for antibody production, which is known to be best in dying cells. So the expected specific anti-FIX antibody concentration in the supernatant may be in the range of 10⁻¹² to 10⁻¹⁴ M. This explains why incubation periods had to be extended compared to standard FVIII assays.

[0047] Results of a screening for an IgG mediated FVIII-like activity in hybridoma cell culture supernatants of a master plate are shown in Fig. 2. Supernatants were examined in a chromogenic FVIII assay. Shown are the results derived from the fifth master plate of fusion experiment number #193 (Balb/c mice immunized with FIXα). Absorbance was read after 4 hours of incubation at 37 °C. Position ES was identified as exhibiting FVIII like activity significantly higher than the blank (MLW). This cell pool was designated 193/C0 and was further subcloned (Figure 3). As each well of the master plate contains more than one hybridoma cell clone, cells of a single positive well were expanded and plated at a calculated cell density of 2 - 0.2 cells/well on a 96 well plate. Again, the supernatants were tested for FVIII-like activity and positive positions were subjected to another round of subcloning. Typically three to four rounds of subcloning were performed with each clone displaying FVIII-like activity to obtain homogenous cell populations. Here the results of the chromogenic assay of the 193/C0 subclones are shown. Absorbance was read after a 4 hour incubation period at 37 °C. Positions A6 and D5 exhibited substantial FVIII-like activity and were named 193/M1 and 193/P1, respectively. These two clones were subjected to another round of subcloning. As a negative control plain cell culture medium was assayed on each plate (MLW(H1)).

[0048] A comparison of chromogenic FVIII-like activity and FIX-ELISA reactivity of small scale (3 ml) hybridoma cultures is shown in Fig. 4. Before a decision was made whether a master clone (or subclone) was to be further subcloned, clones were grown at a 3-5 ml scale and the supernatants were checked again. This graph shows the FIX specific ELISA results and the FVIII-like chromogenic activity of the master clone 193/C0 and all its subclones which were identified as positives and rechecked. Blanks (absorbency of the chromogenic reagent itself) were subtracted in the case of the ELISA as well as the chromogenic assay readings depicted here. Clone 193/M1 was subcloned and yielded clones 193/V2,

193/M2 and 193/U2. The other clones of the 2nd round came from 193/P1, 193/AB2 and 193/P2 were subcloned. 193/AF3, 193/AB3 and 193/AE3 are subclones of 193/AB2. The other clones of the 3rd round came from 193/P2. Finally 193/AF3 (→193/AF4), AE3 (→193/AE4, 193/AL4, 193/AN4 and 193/AO4) and 193/AD3 (→193/AG4, 193/AH4, 193/AD4, 193/AI4, 193/AK4) were subcloned.

[0049] From each fusion experiment, several (5-15) master clones (selected from the master plate) were identified and subjected to subcloning. After 3 rounds of subcloning, most of the cell lines were homogenous as demonstrated by ELISA and chromogenic activity analysis (see Fig. 4) as well as by cDNA sequence analysis. A specific master clone and all its subclones produce the same FIX/FIXa binding antibody. However, there are huge differences in the antibody protein sequences of clones derived from different master clones (see Example 11). Most hybridoma cell lines express antibodies from the IgG subclass (i.e. clones #193, #198, like 198/A1, 198/B1, 198/BB1). However, we were also able to select some clones expressing IgM antibodies.

[0050] The chromogenic activity of hybridoma supernatant of some important master clones and subclones was determined. Absorbance was measured after a 1h 30 min and 3h 30 min incubation period at 37 °C (Fig. 5). In contrast to all the clones from the 193rd fusion, clone 196/C0 and its subclone 196/AP2 produced a FIX/FIXa-specific IgM antibody that gave a strong chromogenic activity even after a short period of incubation.

[0051] The following cell lines have been deposited with the European Collection of Cell Cultures (ECACC) in accordance with the Budapest Treaty: 98/B1 (ECACC No. 99090925); 198/A1 (ECACC No. 99090924); 198/BB1 (ECACC No. 99090926); 193/AO (ECACC No. 99121614); 196/C4 (ECACC No. 99121615); 198/D1 (ECACC No. 99121616); 198/T2 (ECACC No. 99121617); 198/G2 (ECACC No. 99121618); 198/AC1 (ECACC No. 99121619); and 198/U2 (ECACC No. 99121620).

[0052] To do a more in depth analysis of the biochemical properties of certain antibodies, homogenous hybridoma cell lines expressing different antibodies with FVIII-like activity were expanded and used to express the antibody in question on a larger scale (100-1000 ml). These antibodies were affinity purified (see Example 3) prior to being used in further experiments.

Example 3: Factor IX/FIXa_(α,β) binding properties of antibodies exhibiting FIX/FIXa activating activity

[0053] Factor IX and the two activated forms of FIX, FIXα and FIXβ (FIX/FIXa_(α,β)) were diluted in TBS (25mM Tris HCl, 150mM NaCl, pH 7.5) to a final concentration of 2μg/ml. Nunc Maxisorp ELISA plates were coated with 100μl FIX/FIXa_(α,β) solution according to standard procedures (4 °C, overnight) and washed several times with TBST (TBS, 0.1% (v/v) Tween 20). 50μl hybridoma supernatant was diluted 1:1 with 50μl TBST/2%BSA and added to the coated ELISA plate. After an incubation period of 2h at room temperature (RT), plates were washed 4 times with TBST and incubated (2h, RT) with 100μl/well of a 1:25000 dilution (in TBST/1%BSA) of an anti-mouse IgG (Fc-specific) peroxidase conjugated antibody (Sigma, #A-0168). Wells were washed 5 times with TBST and finally stained with 100μl freshly prepared staining solution (10ml 50mM sodium citrate, pH 5 supplemented with 100μl OPD (60mg OPD/ml) and 10μl 30% H₂O₂). The reaction was stopped by the addition of 50ml H₂SO₄ and the optical density recorded at 492nm and 620nm in a Labsystems iEMS Reader MFTM microtiter plate reader employing GENESISTM software.

[0054] In certain cases, instead of an anti-mouse IgG ELISA, an anti- mouse IgM ELISA was carried out.

Purification of mouse-IgG from hybridoma cell culture supernatants

[0055] Hybridoma supernatant (100-500 ml) was supplemented with 200 mM Tris/HCl buffer (pH 7.0) and solid NaCl to give final concentrations of 20 mM Tris and 3M NaCl, respectively. The supernatant was then clarified by centrifugation at 5500 x g for 10 minutes. A 1 ml protein G affinity chromatography column (Protein G Sepharose Fast Flow, Amersham-Pharmacia) was washed with 15 ml 20 mM Tris/Cl pH 7.0 and afterwards equilibrated with 10 ml of 20 mM Tris/Cl buffer pH 7.0 containing 3M NaCl. The hybridoma supernatant containing 3M NaCl was then loaded onto the column by gravity. The column was washed with 15 ml of 20 mM Tris/Cl buffer, pH 7.0, containing 3M NaCl. Bound IgG was further eluted with 12 ml glycine/HCl buffer pH 2.8 and 1 ml fractions were collected. 100μl of 1M Tris pH 9.0 were added to each fraction for neutralization. Fractions containing the IgG were identified by mixing 50μl with 150μl of a staining solution (BioRad concentrate, 1:5 diluted with water) in wells of a microplate. Positive fractions were pooled, concentrated to 1 ml in an ultrafiltration concentrator device (Centricon Plus 20, Amicon) according to the manufacturer. The concentrate was diluted with 19 ml TBS (20 mM Tris/Cl buffer pH 7.0 containing 150mM NaCl) and again concentrated to 1 ml. The diluting-concentrating step was repeated for two more times in order to bring IgG into TBS.

Purification of mouse-IgM from hybridoma cell supernatants

[0056] 100-500 ml of hybridoma cell culture supernatant were concentrated to 5-10 ml either, with an ultrafiltration concentrator device (Centricon Plus 20, Amicon) according to the manufacturer or by ammonium sulfate precipitation

(40% saturation, 0°C) and redissolving the precipitate with 5-10 ml of TBS. In either case the concentrate was dialyzed against 20mM Tris Cl buffer pH 7.4 containing 1.25M NaCl and further concentrated to 1 ml in a Centricon Plus 20, (Amicon) ultrafiltration device. IgM was purified from this concentrate with the ImmunoPure IgM Purification Kit (Pierce) according to the manufacturer. Fractions collected during elution from the maltose binding protein-column were tested for IgM, pooled, concentrated and brought into TBS as described for IgG.

Determination of IgG concentrations in purified preparations

[0057] Total IgG content 280nm - extinction of appropriate dilutions were measured. E280 = 1.4 corresponds to 1 mg/ml protein.

Factor IXa specific IgG (quantitative ELISA)

[0058] Wells of a microplate (Nunc Maxisorp) were incubated with 2µg/ml factor IXa diluted in TBS (25mM Tris/HCl pH 7.5 containing 150mM NaCl) overnight at 4°C. Wells were washed four times with TBST (25mM Tris/HCl pH 7.5 containing 150mM NaCl and 0.1% (v/v) Tween 20). As a standard monoclonal AB the HIX1 anti-FIX (accurate) was used. Standard and samples were diluted in TBST containing 2% (w/v) BSA. The standard dilution series and appropriate dilutions of the samples were incubated on the ELISA-plate for 2 hours at room temperature. Plates were washed 4 times with TBST and incubated (2h, RT) with 100µl/well of a 1:25000 dilution (in TBST/1%BSA) of an anti-mouse IgG (Fc-specific) peroxidase conjugated antibody (Sigma, #A-0168) FIXa. Wells were washed 5 times with TBST and finally stained with 100µl freshly prepared staining solution (10ml 50mM sodium citrate, pH 5 supplemented with 100µl OPD (60mg OPD/ml) and 10µl 30% H₂O₂). The reaction was stopped by the addition of 50ml H₂SO₄ and after 30 minutes the optical density was recorded at 492nm and 620nm in a Labsystems iEMS Reader MF™ microtiter plate reader employing GENESIS™ software.

Example 4: Anti-FIX/FIXa antibodies exhibiting FVIII-like activity in a chromogenic FVIII assay

[0059] Several anti-FIX/FIXa antibody producing hybridoma clones were subcloned up to four times and the resulting monoclonal hybridoma cell line used to produce monoclonal antibody containing supernatant. IgG isotype antibodies derived from these supernatants were purified over affinity columns and dialyzed against TBS (see above). IgM antibodies were used as unpurified supernatant fractions. The following experiments were done with two sets of representative antibodies: 193/AD3 and 198/AC1/1 (IgG isotype, the antibody 198/AC1/1 is a preparation from the parent 198/AC1 hybridoma clone, i.e. that a (frozen) vial containing 198/AC1 cells is cultivated and antibodies are produced. The supernatant is then used for these experiments.) and 196/AF2 and 196/AF1 (IgM isotype) (Fig. 6A and Fig. 6B). Briefly, 25µl aliquots of monoclonal antibody containing sample (unpurified hybridoma supernatant or, where indicated, a certain amount of FIX specific antibody) were transferred to microtiter plate wells and warmed to 37°C. Chromogenic substrate (S-2222), synthetic thrombin inhibitor (I-2581), factor (F) IXa and FX were reconstituted in sterile water and FIXa/FX was mixed with phospholipids according to the supplier's protocol. Per reaction, 50µl of the phospholipid/FIXa/FX solution were combined with 25µl CaCl₂ (25mM) and 50µl of the substrate/inhibitor cocktail. To start the reaction, 125µl of the premix were added to the monoclonal antibody solution in the microtiter plates and incubated at 37°C. Absorbance at 405nm and 490nm of the samples was read at various times (5min to 6h) against a reagent blank (cell culture medium instead of hybridoma supernatant) in a Labsystems iEMS Reader MF™ microtiter plate reader using GENESIS™ software.

[0060] The time course of FVIII-like activity exhibited by monoclonal antibodies 193/AD3 (IgG isotype) and 196/AF2 (IgM isotype) compared to human FVIII (12 and 16mU/ml), TBS and to cell culture medium is shown in Fig. 6A. After a lag phase, both antibodies give rise to chromogenic substrate cleavage, as judged by the increasing optical density measurable at 405nm wavelength.

[0061] The time course of FVIII-like activity exhibited by monoclonal antibodies 198/AC1/1 (IgG isotype, 10µg/ml) and 196/AF1 (IgM isotype, unpurified supernatant) compared to human FVIII (16mU/ml) and 10µg/ml of mouse IgG is shown in Fig. 6B. After a lag phase, both antibodies give rise to chromogenic substrate cleavage, as judged by the increasing optical density measurable at 405nm wavelength.

Example 5: FVIII-like activity exhibited by anti-FIX/FIXa-antibodies generates factor Xa and is phospholipid, FIXa/FX and Ca²⁺ dependent.

[0062] Factor VIII activity is usually determined with a chromogenic assay and/or an APTT-based clotting assay. Both types of assays rely on FVIIIa/FIXa-mediated factor Xa generation. In the case of a chromogenic FVIII assay, the factor Xa produced will subsequently react with a chromogenic substrate, which can be monitored spectroscopically, e.g., in an ELISA reader. In an APTT based clotting assay free factor Xa will assemble with FVa on a phospholipid surface in

the so-called prothrombinase complex and activate prothrombin to thrombin. Thrombin in turn gives rise to fibrin generation and finally to clot formation. Central to the two assay systems is generation of factor Xa by the FVIIIa/FIXa complex. To demonstrate that the FVIII-like activity exhibited by anti-FIX/FIXa-antibodies indeed generates factor Xa, the following experiment was carried out. Several 25 μ l aliquots of unpurified hybridoma supernatant 196/AF2 (IgM isotype) were transferred to microtiter plate wells and warmed to 37 °C. As a positive control, 16mU of Recombinate™ were diluted into hybridoma medium (196 HM 007/99) and treated exactly the same way as the hybridoma supernatant. As a negative control, plain hybridoma medium was used. Chromogenic substrate (S-2222), synthetic thrombin inhibitor (I-2581), factor IXa and FX were reconstituted in sterile water and FIXa/FX was mixed with phospholipids according to the supplier's protocol. Pefabloc Xa®, a factor Xa specific proteinase inhibitor (Pentapharm, LTD), was reconstituted with water to a final concentration of 1mM/l. Per reaction, 50 μ l of the phospholipid/FIXa/FX solution were combined with 25 μ l CaCl₂ (25mM) and 50 μ l of the substrate/thrombin-inhibitor cocktail. To start the reaction, 125 μ l of the premix were added to the samples in the microtiter plates and incubated at 37 °C. Where indicated, 35 μ M Pefabloc Xa® were added. Absorbance at 405nm and 490nm was read at various times (every 5 minutes to 6h) against a reagent blank (cell culture medium) in a Labsystems iEMS Reader MF™ microtiter plate reader employing the GENESIS™ software.

[0063] The results of the factor IXa stimulation by the FVIII-like activity exhibited by the IgM anti-FIX/FIXa-antibody 196/AF2 in generating factor Xa as judged by the readily measurable cleavage of the chromogenic substrate S-2222 (compare "16mU FVIII" and "196/AF2") is shown in Fig. 7A. Factor Xa activity is effectively blocked by the FXa specific inhibitor "Pefabloc Xa®" (compare "196/AF2" versus "196/AF2 35 μ M Pefabloc Xa®") indicating that indeed FXa was generated.

[0064] The same experiment was performed using purified IgG preparations of clone 198/AM1 (Fig. 7B). Purified IgG was diluted in TBS to a final concentration of 0,4mg/ml and 25 μ l (i.e. a total of 10 μ g), transferred to microtiter plate wells and warmed to 37 °C. As a positive control, 6mU plasma-derived FVIII was used. 10 μ g unspecific mouse IgG (Sigma, I-5381) served as a negative control. The assay was performed as described above.

[0065] Further experiments show the factor IXa stimulation by the FVIII-like activity exhibited by the IgG anti-FIX/FIXa-antibody 198/AM1 generates factor Xa as judged by the readily measurable cleavage of the chromogenic substrate S-2222 (Fig. 7B). Again factor VIII and antibody 198/AM1 generate FXa which is effectively blocked by the FXa specific inhibitor "Pefabloc Xa®". As a negative control, unspecific mouse IgG (Sigma, I5381) was assayed.

[0066] In another set of experiments, the dependence of the FVIII-like activity of either purified anti-FIX/FIXa-antibodies (IgM, Fig.8A) or of unpurified antibodies derived from cell culture supernatants (IgG, Fig. 8B) on the presence of phospholipids (PL), FIXa/FX and Ca²⁺ was demonstrated. Mouse IgG was used as a control (Fig. 8C). Factor VIII-like activity was assayed essentially as described above. When indicated, either the FIXa/FX mixture, the PL or Ca²⁺ was omitted from the reaction. Absorbency at 405nm and 490nm of the samples was read at various times against a reagent blank (buffer instead of purified antibody) in a Labsystems iEMS Reader MF™ microtiter plate reader. The results are shown in Fig. 8A, Fig. 8B and Fig. 8C.

[0067] The dependence of the FVIII-like activity of purified anti-FIXa-antibody 198/AC1/1 (IgG isotype, concentration used throughout the assay was 10 μ g/ml) on the presence of phospholipids (PL), FIXa/FX and Ca²⁺ is further shown in Fig. 8A. As is easily recognizable, only the complete assay, including antibody, PL, Ca²⁺, and FIXa/FX gives rise to a reasonable FXa generation. The dependence of the FVIII-like activity of cell culture supernatant containing unpurified IgM isotype anti-FIX/FIXa-antibody (196/AF1) on the presence of phospholipids, FIXa/FX and Ca²⁺ is shown in Fig. 8B.

[0068] Again, as already shown for the purified IgG preparation (Fig. 8A), antibody 198/AC1/1, only the complete assay, including PL, Ca²⁺, FIXa/FX, will give a reasonable amount of FXa generation. To demonstrate the specificity of the reaction, total IgG prepared from normal mouse plasma was assayed under the same conditions as above. The results are shown in Fig. 8C. No FVIII-like activity could be detected. There is, as expected, no activity detectable in the absence of phospholipids, FIXa/FX and Ca²⁺. All experiments were done in a microtiter plate and the OD405 was scanned every 5 minutes for 6h.

Example 6: Certain anti-FIX/FIXa-antibodies are procoagulant in the presence of FIXa

[0069] During normal hemostasis, FIX becomes initially activated either by the tissue factor (TF)/factor VIIa pathway or later on by activated factor XI (FXIa). Subsequent to its activation, FIXa associates on the platelet surface in a membrane bound complex with activated FVIII. Factor IXa by itself has little or no enzymatic activity towards FX, but becomes highly active in the presence of FVIIIa. To demonstrate that certain anti-FIX/FIXa antibodies have FVIII-like activity and hence are procoagulant in a FVIII deficient human plasma, the following experiment was carried out. Different amounts of antibody 193/AD3 or mouse IgG (as a control) were used in a standard aPTT based one stage clotting assay. Briefly, 100 μ l of antibody-containing samples were incubated with 100 μ l of FVIII deficient plasma (DP) and with 100 μ l of DAPTTIN (PTT Reagent for determining activated Thromboplastin Time; IMMUNO AG) reagent, in a KC10A clotting analyzer. Where indicated, a total amount of 50ng activated FIX was included in the reaction mixture. After a 4 minute incubation, the reaction was started by the addition of 100 μ l CaCl₂ (25mM). The results are shown in Table 1 and Fig. 9.

Table 1: Clotting times of FVIII deficient plasma in an APTT based clotting assay employing various amounts of procoagulant (193/AD3) and control antibody (mouse IgG) in the presence of 50ng activated FIX (0.01U FIX). The molar ratio of antibody in the reaction and activated FIX is 10:1. The molar ratio between antibody and total FIX (FIX and FIXa, assuming that human FVIII deficient plasma contains 1U (5 μ g) FIX) varies between 6:1 (9 μ g antibody in reaction) and 1:6 (0.23 μ g antibody in reaction). At the optimal shortening of the clotting time, the molar ratio between antibody and total FIX is 1:1. The clotting time without the addition of FIXa is in the range of 120 seconds.

clotting time (sec)		
μ g AB	193/AD3	mouse IgG
	50ng FIXa	50ngFIXa
9	101.6	102.5
4.5	95.6	103.2
2.25	93.1	103.2
1.8	93.7	101.9
1.35	91.4	103.4
0.9	94.4	102.2
0.45	98.1	101.9
0.34	97.1	103.9
0.23	99.3	103.7

[0070] Fig. 9 is a graphical representation of the clotting times of FVIII deficient plasma in an aPTT based clotting assay employing various amounts of procoagulant (193/AD3) and control (mouse IgG) antibody in the presence of 50ng activated FIX. There is a clear dose-dependent reduction of the clotting time in samples supplemented with antibody 193/AD3. These results imply that antibody 193/AD3 is procoagulant in the presence of FIXa.

Example 7: Anti-FIX/FIXa-antibodies are procoagulant in the presence of FVIII inhibitors and FIXa

[0071] A severe complication of the standard FVIII substitution therapy is the development of alloantibodies directed against FVIII, leading to FVIII neutralization and a condition where the patient's blood will not clot.

[0072] To demonstrate that certain anti-FIXa-antibodies have FVIII-like activity even in the presence of FVIII inhibitors, the following experiment was carried out. Different amounts of antibody 193/AD3 or, as a control, mouse IgG were used in a standard APTT based one-stage clotting assay. Briefly, 100 μ l antibody samples were incubated with either 100 μ l of FVIII deficient plasma (Fig. 10A) or FVIII inhibitor plasma (inhibitor potency 400BU/ml), Fig.10B) as well as with 100 μ l of DAPTTIN reagent, in a KC10A clotting analyzer. In addition, a total amount of 50ng activated FIXa was included in the reaction mixture. After a 4 minute incubation, the reaction was started by the addition of 100 μ l CaCl₂ (25mM). To ensure equal conditions, the experiments employing FVIII deficient plasma and FVIII inhibitor plasma were done side by side. The results are shown in Fig. 10A and 10B. As already shown in Example 6, there is a clear dose-dependent reduction of the clotting time in samples supplemented with antibody 193/AD3 in the presence of FVIII inhibitors.

Example 8: Anti-FIX/FIXa-antibodies are procoagulant in the presence of defective FVIII and FIXa

[0073] To demonstrate that certain anti-FIXa-antibodies have FVIII-like activity in the presence of defective FVIII, the following experiment may be carried out. Increasing amounts of antibody 193/AD3 or, as a control, mouse IgG are used in a standard aPTT-based one stage clotting assay. In this clotting assay, a hemophilia A patient's plasma having very low clotting activity due to the presence of defective FVIII (DF8) is used. Briefly, 100 μ l antibody samples are incubated with either 100 μ l of DF8 plasma or FVIII deficient plasma as well as with 100 μ l of DAPTTIN reagent, in a KC10A clotting analyzer. In addition, a total amount of 50ng activated FIXa is included in the reaction mixture. After a short incubation, the reaction will be started by the addition of 100 μ l CaCl₂ (25mM). To ensure equal conditions, the experiment employing FVIII deficient plasma and DF8 plasma is done side by side.

Example 9: Anti-FIX/FIXa-antibodies with procoagulant activity in the presence of FIXa distinguish between human and bovine FIXa

[0074] FIX/FIXa specific monoclonal antibodies selected from the 198th fusion experiment were purified from the respective hybridoma supernatant and quantified as described in Example 3. These antibodies were analyzed in a modified one-stage clotting assay (as described in Example 6) and some showed procoagulant activity.

[0075] The chromogenic activity of these antibody preparations was measured in the following FXa generation kinetic assay: 10 µg of monoclonal antibody (in 25 µl) were transferred to microtiter plate wells and warmed to 37 °C. Chromogenic substrate (S-2222), synthetic thrombin inhibitor (I-2581), factor IXa and FX were reconstituted in sterile water and FIXa/FX (both bovine) were mixed with phospholipids according to the supplier's protocol. Per reaction, 50 µl of the phospholipid/FIXa/FX solution were combined with 25 µl CaCl₂ (25 mM) and 50 µl of the substrate/inhibitor cocktail. To start the reaction, 125 µl of the premix were added to the monoclonal antibody solution in the microtiter plates and incubated at 37 °C. Absorbance at 405 nm and 490 nm of the samples was read at various times (5 min to 2 h) against a reagent blank (25 ml TBS instead of monoclonal antibodies) in a Labsystems iEMS Reader MFTM microtiter plate reader using GENESISTM software. In parallel, the same reactions were performed except that 50 ng human FIXa were added per reaction. Those antibodies that showed procoagulant activity had no chromogenic activity in the case of bovine FIX, but displayed high activity when human FIXa was present.

[0076] Fig. 11 shows the time course of the FVIII-like activity exhibited by the monoclonal antibodies 198/A1, 198/B1 and 198/AP1 with (+) and without (-) addition of 50 ng human FIXaβ. Non-specific polyclonal mouse IgG was used as a control. 198/A1 and 198/B1 show procoagulant activity (similar as 193/AD3 in example 6) whereas 198/AP1 does not. Antibody 198/BB1 had the same activity pattern (data not shown).

[0077] Further monoclonal antibodies selected from the 198th fusion experiment include 198/D1 (ECACC NO. 99121616), 198/T2 (ECACC No. 99121617), 198/G2 (ECACC No. 99121118), 198/U2 (ECACC No. 99121620).

Example 10 : Structure and procoagulant activity of antibody derivatives derived from anti-FIX/FIXa-antibodies; Subcloning antibody variable domains from hybridoma cell lines 193/AD3, 193/K2, 198/A1 and 198/B1 (clone AB2)

[0078] Cloning procedure: Messenger RNA was prepared from 1x10⁶ hybridoma cells of the respective cell line (either 193/AD3, 193/K2, 198/A1 or 198/B1 (clone AB2)) employing the "QuickPrep® Micro mRNA Purification Kit" (Pharmacia) according to the manufacturer's instructions. The corresponding cDNA was produced by retro transcription of mRNA using the "Ready-To-Go-You-Prime-First-Strand Beads kit" (Pharmacia) according to the manufacturer's instructions. Heavy and light chain encoding sequences were converted to the corresponding cDNA employing a set of primers. To reverse transcribe heavy chain-specific mRNA (VH), an equimolar mixture of the oligonucleotides MOCG1-2FOR (5' CTC AAT TTT CTT GTC CAC CTT GGT GC 3') (SEQ.ID.NO. 1), MOCG3FOR (5' CTC GAT TCT CTT GAT CAA CTC AGT CT 3') (SEQ.ID.NO. 2) and MOCMFOR (5' TGG AAT GGG CAC ATG CAG ATC TCT 3') (SEQ.ID.NO. 3) was used (RTmix1). In the same reaction tube, light chain-specific cDNA (VL) was synthesized using primer MOCKFOR -(5' CTC ATT CCT GTT GAA GCT CTT GAC 3') (SEQ.ID.NO. 4).

[0079] The coding sequences for VH were amplified by PCR using the primer-sets depicted in Fig. 12 and the specific cDNA, derived from the reverse transcription mixture (RTmix1) described above, as the template. VK-chain genes were amplified using the primer sets depicted in Fig. 13 and also employing RTmix1 as a template. The VH-PCR product was cleaved SfiI-Ascl and inserted into SfiI-Ascl digested vector pDAP2 (GeneBank accession no.: U35316). The pDAP2-VH constructs obtained thereby were named pDAP2-193AD3/VH, pDAP2-198A1/VH, pDAP2-198AB2/VH (derived from antibody 198/B1) and pDAP2-193/K2/VH, respectively. The plasmids were subsequently cleaved with Ascl-NotI and the corresponding Ascl-NotI digested VK-gene PCR product was inserted. The resultant vectors were designated pDAP2-193/AD3scFv, pDAP2-198/AlsFv, pDAP2-198/AB2scFv (derived from antibody 198/B1) and pDAP2-193/K2scFv and code for the VH-gene and the VL-gene of the monoclonal antibodies 193/AD3, 198/A1, 198/AB2 (derived from antibody 198/B1) and 193/K2. Heavy and light chains are linked by the coding sequence for an artificial, flexible linker (G₄SGGRASG₄S; Engelhardt et al., 1994) and enables expression of the scFv variant of the respective antibody.

[0080] In Fig. 14, the DNA and the deduced protein sequence of the scFv derived from the hybridoma cell line 193/AD3 are depicted. Nucleotides 1 to 357 code for the heavy chain variable domain, nucleotides 358 to 402 code for the artificial flexible linker and nucleotides 403 to 726 code for the light chain variable region. The protein sequence of the CDR3 region of the heavy chain has the sequence YGNSPKGFAY (SEQ.ID.NO. 5) and is given in bold letters. The artificial linker sequence (G₄SGGRASG₄S) is shown.

[0081] In Fig. 15, the DNA and the deduced protein sequence of the scFv derived from the hybridoma cell line 193/K2 is shown. Nucleotides 1 to 363 code for the heavy chain variable domain, nucleotides 364 to 408 code for the artificial flexible linker, and nucleotides 409 to 747 code for the light chain variable region. The protein sequence of the CDR3

of the heavy chain has the sequence DGGHGYGSSFDY (SEQ.ID.NO. 6), and is given in bold letters. The artificial linker sequence (G₄SGGRASG₄S) is shown.

[0082] In Fig. 16, the DNA and the deduced protein sequence of the scFv derived from the hybridoma cell line 198/AB2 (derived from antibody 198/B1) are depicted. Nucleotides 1 to 366 code for the heavy chain variable domain, nucleotides 367 to 411 code for the artificial flexible linker, and nucleotides 412-747 code for the light chain variable region. The protein sequence of the CDR3 region of the heavy chain has the sequence EGGGFTVNWYFDV (SEQ.ID.NO. 7) and is given in bold letters. The artificial linker sequence (G₄SGGRASG₄S) is also shown.

In Fig. 17, the DNA and the deduced protein sequence of the scFv derived from the hybridoma cell line 198/A1 are depicted. Nucleotides 1 to 366 code for the heavy chain variable domain, nucleotides 367 to 411 code for an artificial flexible linker, and nucleotides 412-747 code for the light chain variable region. The protein sequence of the CDR3 region of the heavy chain has the sequence EGGGYVNWYFDV (SEQ.ID.NO.8) and is given in bold letters. The artificial linker sequence (G₄SGGRASG₄S) is also shown.

Example 11: Procoagulant activity of peptides derived from CDR3 regions of anti-FIX/FIXa-antibodies

[0083] In principle, the antibody molecule can be envisioned as a biological device for the presentation of a combinatorial array of peptide elements in three dimensional space (see Gao et al., 1999, PNAS, 96:6025). Therefore, an antibody (or an antibody derivative, e.g. scFv, Fab, etc.) can be used either as a tool for the detection of functionally important domains of a specific target protein, or on the other hand, for the delineation of amino acid sequences specifically mediating certain interactions, i.e. activating or enhancing the activity of FIXa towards the physiological substrate FX. The latter process has led to the evaluation of a number of heavy chain CDR3 region (CDR3_H) derived peptide sequences as FIXa enhancing agents.

[0084] Enhancing the procoagulant activity of peptides which exhibit such activity may be accomplished through sequence variation within the peptide regions critical for mediating the FIXa activity enhancement. As a possible step towards peptide sequences with enhanced procoagulant activity, the binding site of an antibody, i.e. 198/A1 or 198/B1, on the FIXa molecule is mapped by employing sequence comparison analyses, competitive binding assays, Western blot analyses and competitive ELISA analyses. Since the crystal structure of FIX is known, molecular modeling is subsequently used to improve the fitting of i.e. 198/B1 derived peptides in the 198/B1 binding site on human FIXa.

[0085] On the other hand, methodical mutational analysis of a given peptide sequence such as 198/A1 or 198/B1 CDR3_H derived peptide sequences by, e.g., "alanine scanning mutational analysis" allows for the identification of peptide residues critical for procoagulant activity. Another way to improve the activity of a certain peptide sequence is the use of peptide libraries combined with high throughput screening.

The antigen binding site of an antibody is derived from the juxtaposition of the six "complement determining regions (CDR's)" at the N-terminal end of the VL-HL dimer (or Fv region). The contribution of a single CDR to the antibody specificity for a given antigen may vary considerably, but in general it is thought that the CDR3 region of the heavy chain (CDR3_H) is of special influence, i.e. the particular protein sequence of CDR3_H region may be highly important for antigen recognition. The length of CDR3_H regions has been reported to vary considerably and is in the range of 4-25 amino acids (Borrebaeck, p.16).

An example of a methodical mutational analysis of peptide sequences is given below. To improve the solubility/procoagulant efficacy of peptides derived from the CDR3-region of anti FIX/FIXa antibodies, the N-terminal as well as the C-terminal amino acid sequences were changed. In addition, a series of mutated peptides was constructed and analyzed. The principle of such a study is exemplified by a series of peptides derived from CDR3_H region of antibodies 198/A1 and 198/B1. The original peptide A1 (see table 2) is derived from the CDR3_H region of antibody 198/A1 and peptide B1 is derived from the CDR3_H region of antibody 198/B1, respectively (see example 10, Fig. 16 and 17). The term "scrambled version" means that a peptide has the same amino acids but in random order.

Table 2 List of a series of antibody 198/A1 derived peptides. Listed are the length of the peptide (aa, amino acids #), the calculated molecular weight (MW, in Dalton (D)) and the statistical isoelectric point (pI). D-Arg is abbreviated as Rd.

Peptide	Sequence	Amino-acids	MW (D)	pI	Remark
A1	EGGGYYVNWYFDV (SEQ.ID.No. 9)	(13aa)	1569	7,2	Decreased solubility
A1/1	VYGFGWGYEVNDY (SEQ.ID.No. 10)	(13aa)	1569	7,1	Scrambled version of A1,

(continued)

Peptide	Sequence	Amino-acids	MW (D)	pI	Remark
A1/2	EEEEGGGYVNWYFDEEE (SEQ.ID.No. 11)	(18aa)	2244	5,8	Acidic pI, soluble,
A1/3	RRREGGGYYVNWYFDRRR (SEQ.ID.No. 12)	(18aa)	2407	9,9	Basic pI, soluble,
A1/4	EYGEGYGEVNEYDEFWE (SEQ.ID.No. 13)	(18aa)	2244	5,8	Scrambled version of A1/2
A1/5	VRYNRYRWGYRGRFGDE (SEQ.ID.No. 14)	(18aa)	2407	9,9	Scrambled version of A1/3
A1/3-scr3	RRRGEYGVYWNGDFYRRR (SEQ.ID.No. 15)	(18aa)	2407	9,9	Scrambled version of A1/3
A1/3-Rd	RdRdRdEGGGYYVNWYFDRdRdRd (SEQ.ID.No. 16)	(18aa)	2407	9,9	Peptide A1/3 but substitute D-Arg for L- Arg
A1/3-Rd-srmb	RdRdRdGEYGVYWNGDFYRdRdRd (SEQ.ID.No. 17)	(18aa)	2407	9,9	Scrambled version of A1/3-Rd

[0086] In a first series of experiments we improved the solubility of the original CDR_{3H} peptide sequence (A1; EGG-GYYVNWYFDV) by removing the C-terminal Val residue and adding several charged residues at the N- as well as the C-terminal end of the peptide. The resulting peptides, A1/2 (acidic pI), A1/3 (basic pI) and their respective scrambled versions A1/4, A1/5 and A1/3scr3 were readily soluble in a variety of buffer systems at physiological pH.

[0087] To analyze the FVIII-like (FIXa activating) activity of the peptides, an assay system based on a commercial available FVIII assay was developed (see examples 2 and 4). The basic principle is, that without a cofactor, FIXa will have very limited activity towards its natural substrate FX. Only in the presence of a substance having FIXa activation properties, i.e. FVIII or a substance exhibiting FVIII-like activity, a substantial amount of FXa is produced by cleavage of FX through the FIXa/activator complex. The amount of FXa generated is monitored by cleavage of a chromogenic substrate. The principle of the revised chromogenic assay is described for two representative peptides: A1/3 and A1/5 (Table 2). Briefly, 25 µl aliquots of peptide stock solution (in imidazole buffer (IZ) 50mM imidazole, 100mM NaCl, pH7.2) were transferred to microtiter plate wells and warmed to 37 °C. Chromogenic FXa substrate (S2222), synthetic thrombin inhibitor (1-2581), bovine FIXa and bovine FX were reconstituted in sterile water and FIXa/FX mixed with phospholipids according to the supplier's protocol. Since the peptides do not react with bovine FIXa, (which comes as a mixture with bovine FX in the Test Kit) 2,9nM (in most cases 2.3nM) human FIXa (ERL) were added (see Example 11, Fig 19). Per reaction, 50 µl of the phospholipid /FIXa/FX solution were combined with 25 µl CaCl₂ (25mM) and 50 µl of the substrate/inhibitor cocktail. To start the reaction, 125 µl of the premix were added to the peptide solution in the microtiter plate and incubated at 37 °C. Absorbance at 405nm and 490nm of the samples was read at various times (5 min to 2h) against a reagent blank in a Labsystems iEMS Reader MF™ microtiter plate reader using GENESIS™ software. The result of this experiment are shown in Example 11, Fig 18. Peptide A1/3 induced a readily measurable FXa generation in the presence of 2.9nM human FIXa, whereas the scrambled version A1/5 was inactive. In addition, the acidic peptide A1/2 as well as the scrambled versions A1/4 and A1/3-scr3 did not give any significant chromogenic activity when tested under comparable conditions (data not shown). To prove that the peptide A1/3 like the parental antibody 198/A1 does not react with bovine FIXa and FX the experiment shown in Fig. 19 was done. The peptide A1/3 was incubated as described above with (A1/3 (24 µM), +hFIXa) and without (A1/3 (24 µM), w/o hFIXa) 2.3nM human FIXa (hFIXa). In a control experiment we added plain dilution buffer (IZ) supplemented with 2.3nM hFIXa to the reaction mixture. As shown in Fig. 19, the reaction takes place only in the presence of human FIXa.

Fig. 18 demonstrates the chromogenic FVIII-like activity of peptide A1/3 in the presence of 2.9nM human FIXa (hFIXa). The scrambled version of peptide A1/3, peptide A1/5 does not give rise to any FXa generation. Fig. 19 demonstrates

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the dependence of the chromogenic FVIII-like activity of peptide A1/3 on the presence of human FIXa (hFIXa). In the absence of human FIXa, peptide A1/3 does not give rise to any FXa generation. The buffer control, plain imidazole buffer is designated IZ.

[0088] The peptides were also analyzed for their potential to reduce the clotting time in a FVIII deficient plasma. The aPTT based one stage clotting assay was essentially done as described (see example 6). Clotting times (time from starting the reaction to the "clot"-formation were compared either against FVIII, a buffer control (IZ) or a control peptide (scrambled version). The results of two typical clotting experiments done with two different aPTT reagents (DAPTTIN and Pathromtin SL) are shown in table 3A and table 3B.

Table 3A. Clotting activity of peptides A1/3 and A1/3-scr (scrambled version of A1/3) in FVIII deficient plasma either in the presence or in the absence (w/o) of 2.2nM human FIXa. Shown are two independent representative experiments (Exp. 1 and Exp. 2). All clotting experiments have been done in duplicate. Given are the clotting times for the individual experiments and the average clotting time in seconds (sec). Experiments shown in table 3A have been done employing the aPTT reagent DAPTTIN (Baxter Hyland Immuno). Compared to the buffer control (IZ, imidazole buffer) the peptide A1/3 gave rise to a dose dependent reduction in the clotting time. The reduction in the clotting time became much more pronounced by the addition of 2.2nM activated human FIX to the reaction mix. The scrambled version of peptide A1/3, A1/3-scr3 did not show any reduction of the clotting time. In fact, at concentrations above 2.5 μ M, the scrambled peptide became inhibitory and therefore prolonged the clotting time. Peptides A1/1, A1/2, A1/4 and A1/5 did not give any reduction in the clotting time indicating that they lack procoagulant activity (data not shown).

Exp.1	peptide conc.	w/o FIXa sec	w/o FIXa sec	average sec	2.2nM FIXa sec	2.2nM FIXa sec	average sec
IZ	0	107,7	106,8	107	93,1	94,5	94
A1/3	15 μ M	78,2	77,1	78	59,3	59,9	60
	12,5 μ M	80,2	80,6	80	60,2	58,9	60
	7,5 μ M	97,8	97,9	98	73,1	72,7	73
	2,5 μ M	105,2	104,8	105	91,1	91	91
A1/3-scr3	15 μ M	122,5	122	122	106,1	105,5	106
	12,5 μ M	116	117,6	117	103,1	104,5	104
	7,5 μ M	114,2	113,9	114	100,8	100,6	101
	2,5 μ M	107,8	107,4	108	96,3	95,2	96
Exp.2	peptide conc.	w/o FIXa sec	w/o FIXa sec	average (sec)	2.2nM FIXa sec	2.2nM FIXa sec	average (sec)
IZ	0	111	109,7	110	94,7	95,5	95
A1/3	12.5 μ M	83,6	85,5	85	56,7	56,7	57
	10 μ M	79,1	78,5	79	63,1	62,5	63
	7.5 μ M	100,1	100,5	100	71,6	73,9	73
	5 μ M	103,4	104,8	104	77	76	77
	2.5 μ M	110,1	108,9	110	88	88,8	88
	1,25 μ M	108,7	109,3	109	90,7	90,8	91

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Table 3B. Clotting activity of peptide A1/3 in FVIII deficient plasma when Pathromtin SL (DADE Behring) is used as an aPTT reagent. The experiments were done in duplicate, either in the presence or in the absence (w/o) of 2.2nM human FIXa. Given are the clotting times for the individual experiments and the average clotting time in seconds (sec). Factor VIII and imidazole buffer (IZ) were included as positive and negative control respectively.

	Final conc.	w/o FIXa sec	w/o FIXa sec	average sec	2.2nM FIXa sec	2.2n M FIXa sec	average sec
IZ	0	131,8	132,1	132	107,9	108, 7	108
FVIII	12,5mU/ml	68, 9	69	69	52,9	53,6	53
	6,25mU/ml	77,8	77,9	78	58,6	58,9	59
A1/3							
	15µM	152,8	149,3	151	75,4	75,2	75
	10µM	135,7	134,6	135	76,2	79,8	78
	5µM	152,6	155,6	154	86,6	90,2	88
	1µM	138,3	138,8	139	103,7	105, 9	105

[0089] In contrast to the experiments shown in table 3A the experiments shown in table 3B have been done employing the aPTT reagent Pathromtin SL. In the presence of FIXa, the peptide A1/3 gave rise to a dose dependent reduction in the clotting time whereas in the absence of FIXa no reduction of the clotting time was detectable.

[0090] In another series of experiments we set out to improve the plasma stability (protection from, e.g., proteolytic degradation) of peptide A1/3. One approach was to substitute the N- and C-terminal L-Arg residues with D-Arg residues (exemplified by peptides A1/3-rd and A1/3-Rd-srmb). Peptides A1/3-rd and A1/3-Rd-srmb (scrambled version of the peptide) were then analyzed in a chromogenic as well as in the aPTT based clotting assay. These experiments revealed that exchanging the terminal L-Arg residues for D-Arg residues did not change the FVIII-like activity as measured in the chromogenic assay, indicating that chirality of the Arg-residues does not play a major role in chromogenic activity (Fig. 20). In addition, the aPTT based one-stage clotting activity, although somewhat reduced, was still easily detectable (Table 4).

Table 4 One stage clotting activity of peptides A1/3, A1/3-Rd and A1/3-Rd-srmb (sequences see table 2). IZ, buffer control.

	Peptide conc.	w/o FIXa sec	w/o FIXa, sec	average sec	2.2nM FIXa sec	2.2nM FIXa sec	average sec
IZ	0	110	109,1	110	96	96	96
A1/3	15µM	77,8	78	78	56,1	55,5	56
	12,5µM	99,4	100,5	100	65	68	67
	10µM	104,4	109,5	104	72	73,2	73
	7,5µM	105,2	105,2	105	80,7	80,5	81
	5µM	108,4	107,7	108	89,7	88,3	89
	2,5µM	107,9	107,6	108	93,6	93,3	93
	1,25µM	106,7	107	107	94,4	95	95
A1/3-Rd	15µM	96,4	95,4	96	76,1	74,4	75
	12,5µM	98	98,6	98	72,3	73,7	73
	10µM	93,5	95,8	95	74,2	77,2	76
	7,5µM	97,6	98,1	98	80,9	82,2	82

(continued)

	Peptide conc.	w/o FIXa sec	w/o FIXa, sec	average sec	2.2nM FIXa sec	2.2nM FIXa sec	average sec
5	5 μ M	99,2	99,1	99	86	85,1	86
	2,5 μ M	102,7	103,4	103	94,4	94,7	95
	1,25 μ M	107,5	107,7	108	96,6	96	96
10	A1/3-Rd srmb 15 μ M	121,9	121,3	122	112,7	112,4	113
	12,5 μ M	117,2	118	118	108,1	107,8	108
	10 μ M	115,8	115,3	116	107,2	107,8	108
15	7,5 μ M	114,6	113,6	114	107,6	106,6	107
	5 μ M	113,1	112,4	113	108,5	108,2	108
	2,5 μ M	111,9	111,9	112	105	104,2	105
20	1,25 μ M	107,2	107,1	107	101,1	105,3	103

[0091] Fig. 20 demonstrates the unchanged chromogenic activity of peptide A1/3-Rd. Peptides at a final concentration of 12 μ M or the buffer control (IZ) were incubated in the presence of 2.3nM human FIXa (+). The chromogenic activity of peptide A1/3 and A1/3-Rd was found to be virtually unchanged and gave almost identical results in the chromogenic assay. The scrambled version of peptide A1/3, A1/5 as well as the buffer gave no significant FXa generation.

[0092] In the next series of experiments we set out to determine the individual role of any amino acid of the peptide core sequence by substituting each residue for the amino acid Alanine (Table 5).

Table 5. Listed are the peptides designed to elucidate the role of any single amino acid within the peptide core sequence (E₁G₂G₃G₄Y₅Y₆V₇N₈W₉Y₁₀F₁₁D₁₂). The lower case numbers describe the position of the amino acid within the peptide. Alanine, an uncharged small amino acid, was substituted for each amino acid ("Alanine scan"). Also listed are the lengths of the peptides (amino acids #), the calculated molecular weights (MW, in Dalton (D) and the statistical isoelectric points (pI).

Peptide	Sequence	Amino acid #	MW (D)	pI	Remark
A1/3	RRREGGGYYVNWFDRRR (SEQ.ID.No. 18)	(18aa)	240 7	9, 9	Basic pI, soluble,
A1/3-13	RRR A GGGGYYVNWFDRRR (SEQ.ID.No. 19)	(18aa)	234 9	10 .4	E ₁ -A ₁
A1/3-1	RRRE A GGGGYYVNWFDRRR (SEQ.ID.No. 20)	(18aa)	242 1	9. 9	G ₂ -A ₂
A1/3-2	RRREG A GYYVNWFDRRR (SEQ.ID.No. 21)	(18aa)	242 1	9. 9	G ₃ -A ₃
A1/3-3	RRREGG A YYVNWFDRRR (SEQ.ID.No. 22)	(18aa)	242 1	9. 9	G ₄ -A ₄
A1/3-4	RRREGGG A YVNWFDRRR (SEQ.ID.No. 23)	(18aa)	231 5	9. 9	Y ₅ -A ₅
A1/3-5	RRREGGGGY A VNWFDRRR (SEQ.ID.No. 24)	(18aa)	231 5	9. 9	Y ₆ -A ₆
A1/3-6	RRREGGGGGY A NWFDRRR (SEQ.ID.No. 25)	(18aa)	237 9	9. 9	V ₇ -A ₇
A1/3-7	RRREGGGGGYY A WFDRRR (SEQ.ID.No. 26)	(18aa)	236 4	9. 9	N ₈ -A ₈

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(continued)

Peptide	Sequence	Amino acid #	MW (D)	pI	Remark
A1/3-8	RRREGGGYYVN A YFDRRR (SEQ.ID.No. 27)	(18aa)	229 2	9. 9	W ₉ -A ₉
A1/3-9	RRREGGGYYVN W A ₁₀ FDRRR (SEQ.ID.No. 28)	(18aa)	231 5	9. 9	Y ₁₀ -A ₁₀
A1/3-10	RRREGGGYYVN W Y A DRRR (SEQ.ID.No. 29)	(18aa)	233 1	9. 9	F ₁₁ -A ₁₁
A1/3-11	RRREGGGYYVN W Y F ARRR (SEQ.ID.No. 30)	(18aa)	236 3.5	10.5	D ₁₂ -A ₁₂
A1/3-12srm b	RRRYVYNGWGYFEG A ARRR (SEQ.ID.No. 31)	(18aa)	236 3	10.4	Scrambled version

[0093] Each of the peptides was dissolved individually in imidazole buffer (50mM imidazole, 100mM NaCl, pH7.2) and subsequently diluted in clotting buffer (50mM imidazole, 100mM NaCl, 1% human albumin, pH7.4) to the desired final concentration. The peptides were analyzed for their chromogenic activity as well as for their potential to reduce the clotting time in a FVIII deficient plasma. The one-stage clotting assay was essentially done as described (see example 6). Clotting times (time from starting the reaction to the "clot"-formation) were compared either against a buffer control or a control peptide (scrambled version). Some of the results of the "Alanine scan" are given for the peptides A1/3-2 and A1/3-3. The change of G₃-A₃ as exemplified in the peptide A1/3-2 yields high chromogenic activity and a strong reduction of the one-stage clotting time (34 seconds at a concentration of 12.5μM) in the presence of 2.2nM human FIXa. Peptide A1/3-3 (G₄-A₄) exhibits an optimum of chromogenic activity around a final concentration of 12μM with decreased activity at either higher or lower concentrations. The peptide is somewhat inhibitory in a one-stage clotting assay at higher concentrations (12.5μM) in the absence of FIXa but becomes strongly active in the presence of 2.2nM FIXa (31 seconds, 12.5μM).

[0094] In the next series of experiments we set out to determine the individual role of any amino acid of the peptide core sequence by substituting each core residue for the amino acid glutamic acid (E) (see Table 6).

Table 6. Listed are the peptides designed to elucidate the role of any single amino acid within the peptide core sequence (E₁G₂G₃G₄Y₅Y₆V₇N₈W₉Y₁₀F₁₁D₁₂). The lower case numbers describe the position of the amino acid within the peptide. Glutamic acid, a negatively charged large amino acid, was substituted for each amino acid of the core sequence ("Glutamic acid scan"). Also listed are the lengths of the peptide (amino acids #), the calculated molecular weights (MW, in Dalton (D)) and the statistical isoelectric points (pI).

Peptide	Sequence	Amino-Acids	MW (D)	pI	Remark
A1/3	RRREGGGYYVN W YFDRRR	(18aa)	2407	9,9	Basic pI, soluble,
A1/3-22	RRRE E GGYYVN W YFDRRR (SEQ.ID.No. 32)	(18aa)	2479	9.5	G ₂ -E ₂
A1/3-23	RRRE E GGYYVN W YFDRRR (SEQ.ID.No. 33)	(18aa)	2479	9.5	G ₃ -E ₃
A1/3-24	RRREG E YYVN W YFDRRR (SEQ.ID.No. 34)	(18aa)	2479	9.5	G ₄ -E ₄
A1/3-26	RRREGGG E YVN W YFDRRR (SEQ.ID.No. 35)	(18aa)	2373	9.4	Y ₅ -E ₅
A1/3-27	RRREGGGY E VN W YFDRRR (SEQ.ID.No. 36)	(18aa)	2373	9.4	Y ₆ -E ₆
A1/3-28	RRREGGGYY E N W YFDRRR (SEQ.ID.No. 37)	(18aa)	2437	9.5	V ₇ -E ₇

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(continued)

Peptide	Sequence	Amino-Acids	MW (D)	pI	Remark
A1/3-29	RRREGGGYYV EW YFDRRR (SEQ.ID.No. 38)	(18aa)	2422	9.5	N ₈ -E ₈
A1/3-30	RRREGGGYYV NE YFDRRR (SEQ.ID.No. 39)	(18aa)	2350	9.5	W ₉ -E ₉
A1/3-31	RRREGGGYYV NW EFDRRR (SEQ.ID.No. 40)	(18aa)	2373	9.4	Y ₁₀ -E ₁₀
A1/3-32	RRREGGGYYV NW YEDRRR (SEQ.ID.No. 41)	(18aa)	2389	9.5	F ₁₁ -E ₁₁
A1/3-33	RRREGGGYYV NW YFERRR (SEQ.ID.No. 42)	(18aa)	2421	9.9	D ₁₂ -E ₁₂
A1/3-34srmb	RRRGEYGEYWNGDFYRRR (SEQ.ID.No. 43)	(18aa)	2437	9.5	Scrambled version

[0095] Each of the peptides was solved individually in imidazole buffer (50mM imidazole, 100mM NaCl, pH7.2) and subsequently diluted in clotting buffer (50mM imidazole, 100mM NaCl, 1% human albumin, pH7.4) to the desired final concentration. The peptides derived from the "Glutamic acid scan" series were analyzed for their chromogenic FVIII-like activity as well as for their potential to reduce the clotting time in a FVIII deficient plasma. The one-stage clotting assay was essentially done as described (see example 6).

[0096] The peptide A1/3-24 showed some interesting properties. The molecule exhibited high chromogenic FVIII-like activity at concentrations between 6.5μM-12μM but lost activity at higher concentrations (up to 24μM). The peptide had no procoagulant activity in the absence of human FIXa but was strongly active in the presence of 2.2nM hFIXa. In a second series of experiments we set out to improve the procoagulant activity of the antibody 198/B1 CDR3H derived peptide sequence B1. In a first step we improved the solubility of the original peptide sequence (B1; EGGGFTVNWYFDV) by removing the C-terminal Val residue and adding several charged residues at the N- as well as the C-terminal end of the peptide. The resulting peptides B1/4, B1/6 (acidic pI), B1/7 (basic pI) and their scrambled versions B1/5, B1/7scr3 are readily soluble in a variety of buffer systems at physiological pH.

Table 7 is a list of a series of antibody-198/B1 derived peptides. Listed are the length of the peptide (aa, amino acids #), the calculated molecular weight (MW, in Dalton (D) and the statistical isoelectric point (pI).

Peptide	Sequence	Amino-acids	MW (D)	pI	Remark
B1	EGGGFTVNWYFDV (SEQ.ID.No. 44)	(13aa)	1491	6,0	Decreased solubility
B1/4	REGGGFTVNWYFDR (SEQ.ID.No. 45)	(14aa)	1704	7,9	Soluble,
B1/5	FGVGYRGETRNFDW (SEQ.ID.No. 46)	(14aa)	1704	8,0	Scrambled version, soluble
B1/6	EEEEGGGFTVNWYFDEEE (SEQ.ID.No. 47)	(18aa)	2166	5,0	Acidic pI soluble
B1/7	RRREGGGFTVNWYFDRRR (SEQ.ID.No. 48)	(18aa)	2329	9,9	Basic pI soluble
B1/7scr3	RRRFGVGYGETNFDWRRR (SEQ.ID.No. 49)	(18aa)	2329	9,9	Basic pI, soluble, scrambled version

[0097] Peptides B1/4 and B1/5 were soluble in 50mM Tris, 100mM NaCl, pH=6.5. Both peptides were analyzed in a chromogenic FVIII assay. Peptide B1/4 but not the scrambled version B1/5 was found to have some chromogenic activity

(data not shown).

[0098] Subsequently peptides B1/6, B1/7 and B1/7scr3 were analyzed. Each of the peptides was solved individually in 50mM imidazole, 100mM NaCl, pH7.2 and subsequently diluted either in clotting buffer (50mM imidazole, 100mM NaCl, 1% human albumin, pH7.4) or in imidazole buffer to the desired final concentration. The peptides were analyzed for their chromogenic activity as well as for their potential to reduce the clotting time in a FVIII deficient plasma (table 8 & 9). The one stage clotting assay was essentially done as described (see example 6). Clotting times (time from starting the reaction to the "clot"-formation) were compared either against a buffer control or a control peptide (scrambled version).

[0099] The FIXa activating activity (FVIII cofactor-like activity) from peptide B1/7 was first measured in the chromogenic assay described above.

As shown in Fig. 21, the addition of 2.4 μ M peptide B1/7 to the reaction mixture led to a well measurable generation of FXa. In contrast, the addition of 35 μ M Pefabloc Xa, a specific inhibitor of FXa protease activity, resulted in a significant reduction of the chromogenic substrate cleavage reaction (Fig. 22) thereby proving that there was indeed a peptide-FIXa mediated FXa generation. If there was no addition of FIXa and FX to the reaction mixture, no FXa was synthesized (Fig. 22). Peptide B1/6 and the control peptides B1/5 and B1/7scr3 exhibited no activity (data not shown).

Fig. 21 demonstrates the chromogenic activity of peptide B1/7. The peptide at a final concentration of 2.4 μ M or the buffer control (IZ) were incubated in the presence of 2.3nM human FIXa.

In Fig. 22 peptide B1/7 at a final concentration of 2.4 μ M or the buffer control (IZ) were incubated in the presence of 2.3nM human FIXa (as indicated either as "+2.3nM hFIXa" or "+"). The chromogenic activity of peptide B1/7 was found to be dependent on the presence of FIXa and FX since no reaction is detectable when FIXa and FX are left out of the reaction (w/o FIXa/FX). To prove that the peptide B1/7 mediates indeed FXa generation, the FXa specific protease inhibitor Pefabloc Xa was added to the reaction mix (35 μ M Pefabloc Xa). In a second set of experiments, the procoagulant effect of peptides B1/6, B1/7 and B1/7scr3 were tested in a aPTT based one-step coagulation assay. The experiments were done essentially as described in Example 6. The results are shown in tables 8 and 9.

Table 8: FVIII deficient plasma was incubated either with peptides B1/6, B1/7scr3 or B1/7 in the absence of activated human FIX. As a negative control, plain buffer was added to the deficient plasma. The clotting times for the various combinations are given. Under these conditions, peptide B1/7 at its highest concentration (12.5 μ M) becomes inhibitory to the coagulation process as indicated by the extended clotting time of 157 seconds.

Peptide	12,5 μ M (-)	1.25 μ M (-)	0.125 μ M (-)	12,5nM (-)	Buffer (-)	remarks
B1/6	115	110	111	111	110	
B1/7	157	112	109	110	110	
B1/7scr3	115	105	106	105	107	

Table 9: FVIII deficient plasma was incubated either with peptides B1/6, B1/7scr3 or B1/7 in the presence of activated human FIX. As a negative control, plain buffer was added to the deficient plasma. The clotting times for the various combinations are given. In the presence of FIXa, peptide B1/7 becomes procoagulant as indicated by the reduced clotting time (83 seconds compared to 102 seconds for the scrambled peptide and 100 seconds for the buffer control)

Peptide	12,5 μ M (+)	1.25 μ M (+)	0.125 μ M (+)	12,5nM (+)	Buffer (+)	remarks
B1/6	103	100	101	100	100	
B1/7	83	92	99	99	100	
B1/7scr3	102	94	94	94	94	

Example 12: Procoagulant activity of peptide derivatives obtained from CDR3 regions of anti- FIX/FIXa-antibodies in FVIII inhibitor plasma

[0100] To assay for the procoagulant activity of peptide A1/3 in FVIII inhibitor plasma the following experiment was carried out. We performed a standard aPTT based one stage clotting assay, but instead of FVIII deficient plasma we employed FVIII inhibitor plasma. The inhibitory potency of the plasma was 8.1 Bethesda Units per ml.

Table 10: Various amounts of peptide A1/3 (12.5 μ M-1.25 μ M) were added to FVIII inhibitor plasma (either in the presence (FIXa) of 2.2nM FIXa or in the absence (w/o FIXa). As a negative control, plain buffer was added to the plasma (IZ). Experiments were done in duplicate and the average (aver.) was calculated. The clotting times (in seconds) for the various combinations are given. It is easily appreciable that the peptide A1/3 reduces (in a dose dependent manner) the clotting time of FVIII inhibitor plasma in the presence of FIXa but, although albeit to a much lesser extent, also in the absence of FIXa.

		w/o FIXa	w/o FIXa			FIXa	FIXa	
	Peptide conc.	sec	sec	Average sec		sec	sec	average sec
IZ	0	104,8	103,6	104		94,2	94,1	94
A1/3	12,5 μ M	85,8	85,3	86		61	60,2	61
	10 μ M	88,4	87,9	88		61,3	61,8	62
	7,5 μ M	93,7	92,7	93		68,8	70,9	70
	5 μ M	101, 5	101,1	101		81	82	82
	2,5 μ M	106,1	105,3	106		90,2	90,5	90
	1,25 μ M	104,5	104,3	104		91,3	91,4	91

Example 13: Conversion of the 196/C4 IgM into IgG1

[0101] Since some IgM antibodies demonstrate high FVIII-like activity in chromogenic assays, attempts were made to convert such IgM antibodies into IgG antibodies (though antibody derivatives such as Fab, F(ab)₂, scFv, etc. could also be produced). Described in detail below is the rescue of the IgM variable region genes. Expression vector pBax-IgG1 (Fig. 23) was first constructed from vectors pSI (Promega) and pEF/Bsd (Invitrogen) through multiple cloning steps. B-lymphocytes of a donor are purified from blood and mature mRNA purified from these cells using the "micro-mRNA purification-kit" (Pharmacia). The cDNA of a human kappa chain and a human gamma 1 chain are prepared employing the "you-primefirst-strand-cDNA-"kit" (Pharmacia) using specific primers.

[0102] The coding sequence of a human kappa light chain constant domain is amplified from the cDNA by PCR using specific primers.

[0103] The gene of a human gamma 1 chain constant region (CH1-hinge-CH2-CH3) is amplified from the cDNA by PCR using specific primers.

[0104] The PCR product of the light chain constant domain is digested with XbaI and NheI and inserted into digested pSI. The resultant vector is cleaved with EcoRI and XbaI and annealed oligonucleotides are inserted, resulting in vector pSI-Ckappa. The annealed oligonucleotides provide for the leader and the SacI-XbaI sites for insertion of the kappa chain variable region. The PCR product of the human gamma 1 chain constant region is digested with SpeI and BamHI and inserted into digested pSI. The resultant vector is cleaved with SpeI and NotI and annealed oligonucleotides are inserted resulting in vector pSI-Cgamma. The annealed oligonucleotides provide for the leader and the XhoI-BstEI sites for insertion of the heavy chain variable region. Vector pEF/Bsd is digested NheI and SfiI, blunt ended by Klenow treatment and the whole expression cassette of pSI-Ckappa, excised with BglII and BamHI, is inserted (after Klenow treatment). The resultant vector is digested with EcoRI and HindIII and treated with Klenow. The whole expression cassette of pSI-Cgamma is excised with BglII and BamHI and is inserted (after Klenow treatment). The resultant vector is named pBax-IgG1.

[0105] The light chain variable region can be inserted in between the SacI-XbaI sites, yielding the complete coding-sequence of a kappa light chain. The heavy chain variable region can be cloned in between the XhoI-BstEI sites, resulting in a complete IgG1 heavy chain gene. Both open reading frames are expressed under the control of the SV40-promoter and harbour the coding sequence of a signal peptide at the 5' end of the genes for secretion of the heavy and light chains into the endoplasmic reticulum. Transfection into COS cells allows the expression of an IgG1 with the same binding properties as the parental IgM.

Construction of the plasmid pBax-196/C4 is further accomplished by amplifying the VH of the 196/C4 scFv (subcloned as described in Experiment 10) by PCR using specific primers. The PCR product is digested with XhoI and BstEI and

inserted into XhoI and BstEII digested pBax IgG1. The VL of the 196/C4 scFv is amplified by PCR using specific primers. The PCR product is digested with SacI and XbaI and inserted into SacI and XbaI-digested pBax IgG1-VH. The resultant vector (pBax-196/C4) is transfected into COS cells by electroporation, and hybrid IgG1 molecules (murine variable region and human constant region) with the same specificity as the parental IgM is expressed.

Example 14: Activation of FIXa amidolytic activity by anti-FIXa antibodies:

[0106] Briefly, 20 µl factor IXa (containing 200mU FIXa (Stago)) were incubated at 37 °C, with 200 µl of reaction buffer (50mM TrisHCl pH7.4, 100mM NaCl, 5mM CaCl₂ and 40% Ethyleneglycol), 25 µl of FIXa substrate (CH₃SO₂-D-CHG-Gly-Arg-pNA, AcOH, 10 µM/ml, Pentapharm LTD) in the absence or presence of various amounts of anti-FIX antibodies 198/B1 (IgG isotype) or 196/AF1 (IgM isotype). Specific cleavage of FIXa substrate was monitored at 405nm in an ELISA reader.

The presence of the anti-FIX antibodies enhanced the amidolytic activity of FIXa at least 2 fold.

Fig. 24 shows the increase of the amidolytic activity of FIXa in the presence of antibody 198/B1 (Fig. 24A) and antibody 198/AF1 (Fig. 24B).

Example 15: FVIII-like activity exhibited by Fab fragments derived from anti- FIX/FIXa-antibodies.

[0107] Fab fragments of anti-FIX/FIXa antibodies were prepared and purified according to standard protocols. Briefly, 1ml antibody 198/A1 (4mg/ml in 50mM imidazole, 100mM NaCl, pH7.4) was incubated overnight with 87 µl fragmentation buffer (1M Na Acetate, 10mM EDTA 67.5mg/ml L-cysteine) and 0.25mg papain (immobilized on agarose beads), at 37 °C. The preparation was filtered to remove the papain. L-histidine was added (final concentration 50mM) and afterwards the pH was adjusted to 7.0. Finally, solid NaCl is added to give a final concentration of 1M.

Subsequently, the 198/A1 Fab fragment was purified by binding to protein L: We used ImmunoPure Immobilized PROTEIN L Plus (Pierce) in a PHARMACIA XK 16/20 Column (gel-volume: 2ml) Buffers for chromatography were: 1) equilibration-buffer : 50mM L-histidine pH 7.0; 1M NaCl; 0.1% (w/v) NaN₃; 2) wash-buffer: 50mM L-Histidine pH 7.0; 0.1% (w/v) NaN₃; 3) elution-buffer: 100 mM glycine pH 2.5; 0.1% (w/v) NaN₃; and 4) neutralization buffer: 2M Tris/Cl pH 8.0;

[0108] Chromatography was essentially done by following steps 1 to 7 described in table 11. In order to neutralize the low pH of the elution buffer "Fraction-tubes" were preloaded with 0.2 ml 2M Tris pH 8.0.

Table 11

	STEP	BUFFER	Flow rate	Vol.	CV	Fractions
1.	column-wash	elution-buffer	2,0 ml/min	10 ml	5	waste
2.	equilibration	equi-buffer	2,0 ml/min	10 ml	5	waste
3.	sample-load	sample	1,0 ml/min	x ml	x	flow-through
4.	wash 1	equi-buffer	1,0 ml/min	20 ml	10	flow-through
5.	wash 2	wash-buffer	1,0 ml/min	10 ml	5	flow-through
6.	elution	elution-buffer	1,0 ml/min	15 ml	7,5	1,0 ml fractions-
7.	neutralization	wash-buffer	2,0 ml/min	10 ml	5	waste

[0109] The final 198/A1 Fab preparation was dialyzed against 50mM imidazole, 100mM NaCl, pH7.4 and analyzed in a chromogenic FVIII assay as described above (Fig. 25). Compared to an intact antibody, the 198/A1 Fab fragment has somewhat less activity; however, the Fab fragment still gives rise to FIX dependent FXa generation. Fig. 25 demonstrates the chromogenic FVIII-like activity of the antibody 198/A1 Fab fragment in the presence of 2.3nM human FIXa. As a positive control we used the intact antibody 198/A1 as well as 7.5pM FVIII. Buffer control (IZ) instead of 198/A1 Fab fragment or FVIII was used as a negative control.

Example 16: FVIII-like activity exhibited by fusion proteins between scFv fragments of anti-FIX/FIXa antibodies and E. coli alkaline phosphatase.

[0110] The single chain Fv fragment (see example 10) of antibody 198/B1 (subclone AB2) was fused to the N-terminus of E. coli alkaline phosphatase employing the pDAP2 vector system (Kerschbaumer et al., 1996). Two identical clones were isolated and designated pDAP2-198AB2#1 and pDAP2-198AB2#100 (Fig. 26). The resulting fusion proteins were expressed in E. coli, purified by metal affinity chromatography (Kerschbaumer et al., 1997) and analysed in a standard

chromogenic assay (Fig. 27).

Fig. 27 demonstrates the chromogenic FVIII-like activity of two antibody 198/B1 (subclone AB2) scFv fragment-alkaline phosphatase fusion proteins (198AB2#1 and 198AB2#100) in the presence of 2.3nM human FIXa. As a positive control we used 7.5pM FVIII.

Example 17: FVIII-like activity exhibited by a bivalent miniantibody.

[0111] In order to obtain a bivalent miniantibody, the scFv fragment of antibody 198/B1 (subclone AB2) was fused to a amphipatic helical structure employing the pZip1 vector system (Kerschbaumer et al. (Analytical Biochemistry 249, 219-227, 1997). Briefly, the gene of the 198/B1 scFv fragment was isolated from the plasmid pDAP-198AB2#100 (example 16) by digestion with SfiI and NotI. The DNA fragment was gel purified and inserted in the SfiI/NotI digested vector pzip1. The resulting plasmid was sequenced and designated pZip-198AB2#102 (Fig.28). In parallel, we constructed a miniantibody version from an irrelevant monoclonal antibody termed #8860. In a first step, the single chain Fv fragment of antibody #8860 was assembled in the vector pDAP2. The cloning was done essentially as described in example 10. The construct was named pDAP2-8860scFv#11 (Fig. 29). Subcloning of the scFv fragment contained within pDAP2-8860scFv#11 into plasmid pZip1 (see above) yielded the miniantibody construct p8860-Zip#1.2 (Fig. 30). Since antibody #8860 does not react with FIX/FIXa (as judged by Western Blot and ELISA analysis) it represents an appropriate negative control. Subsequently, the miniantibody proteins were expressed in E. coli and purified from bacterial supernatants by binding to Protein L according to the following protocol: For affinity chromatography we used ImmunoPure Immobilized PROTEIN L Plus (Pierce) in a PHARMACIA XK 16/20 Columns having a gel-volume of 4ml Buffers employed were: 1) equilibration-buffer : 50mM L-Histidine pH 7.0, 1M NaCl, 0.1% (w/v) NaN_3 ; wash-buffer: 50mM L-histidine pH 7.0, 0.1% (w/v) NaN_3 ; elution-buffer: 100 mM glycine pH 2.5, 0.1% (w/v) NaN_3 ; and neutralization buffer: 2M Tris/Cl pH 8.0

[0112] Samples were prepared as follows: The bacterial culture supernatant was obtained by centrifugation of the bacterial expression culture (11,000 x g, 4°C, 10 minutes). 470 g of ammonium-sulphate was added to 1 liter of supernatant and the solution stirred on ice for 1 hour to precipitate the protein. The precipitate was pelleted at 14,000 x g for 35 minutes at 2°C and re-dissolved in 100 ml 20mM Tris pH 7.0. Subsequently the concentrate was dialyzed against 20mM Tris pH 7.0, L-histidine was added to a final concentration of 50mM and the pH was adjusted to 7.0. Finally, solid NaCl was added to give a final concentrations of 1M. Before loading on the column, a sample was first centrifuged at 16,000 x g for 15 min at room temperature and then filtered through a 0.45µm sterile filter.

[0113] Chromatography was essentially done by following steps 1 to 7 described in table 12. In order to neutralize the low pH of the elution buffer "Fraction-tubes" were preloaded with 0.2 ml 2M Tris pH 8.0.

Table 12. The final 198/B1 (subclone AB2) miniantibody preparation (designated 198AB-Zip#102) and the negative control 8860-Zip#1.2 were dialyzed against 50mM imidazole, 100mM NaCl, pH7.4 and analyzed in a chromogenic FVIII assay as described above (Fig. 31).

	STEP	BUFFER	Flow rate	Vol.	CV	Fractions
1.	column-wash	elution-buffer	2.0 ml/min	20 ml	5	waste
2.	equilibration	equi-buffer	2.0 ml/min	20 ml	5	waste
3.	sample-load	sample	1.0 ml/min	x ml	x	flow-through
4.	wash 1	equi-buffer	1.0 ml/min	40 ml	10	flow-through
5.	wash 2	wash-buffer	1.0 ml/min	20 ml	5	flow-through
6.	elution	elution-buffer	1.0 ml/min	30 ml	7.5	1,0 ml fractions-
7.	neutralization	wash-buffer	2.0 ml/min	20 ml	5	waste

[0114] As can be seen in Fig. 31, the miniantibody construct 198AB-Zip#102 gives rise to substantial FXa generation (compare to FVIII) whereas the negative control miniantibody 8860-Zip#1.2 does not. Fig. 31 demonstrates the chromogenic FVIII-like activity of the 198/B1 (subclone AB2) miniantibody 198AB-Zip#102 in the presence of 2.3nM human FIXa. As a positive control we used 4.8pM FVIII whereas an unrelated miniantibody (8860-Zip#1.2) and plain reaction buffer (IZ) served as negative controls.

Example 18: FVIII-like activity exhibited by anti-FIXa/FIX antibody scFv fragments

[0115] The single chain Fv fragment of antibody 198/B1 (subclone AB2) as well as the scFv fragment of antibody #8860 were expressed employing the pMycHis6 vector system. Vector pMycHis6 (Fig. 32 & 33) was constructed by cleaving vector pCOCK (Engelhardt et al., 1994, Biotechniques, 17:44-46) with NotI and EcoRI and insertion of the following oligonucleotides: mychis6-co: 5'ggccgcagaacaaaaactcatctcagaagaggatct gaatggggcggcacatcaccatcaccatcactaataag 3' (SEQ.ID.NO. 79) and mycchis-ic:5'aattcttattagtgatggatggatggatgtgccgccccattcagatcctct tctgagatgagttttgttctgc 3' (SEQ.ID.NO. 80) Fig. 32 shows a schematic representation of the plasmid pMycHis6. The c-myc-tag sequence is used to detect the scFv fragment in an ELISA or a Western Blot analysis (Evan et al., Mol.Cell.Biol., 1985, 5(12), pp. 3610-6). The His6-tag sequence was included to facilitate the purification of scFv fragments by metal ion chromatography (Hochuli et al., 1988, Biotechnology, 6:1321-1325). The plasmid contains the lacZ gene promoter (PlacZ) the PelB-leader sequence (see legend Fig. 26) an E. coli origin of replication (colE1ori) and a M13 phage origin of replication (M13ori). To allow for specific selection, the plasmid also carries the gene for the enzyme β -lactamase (AmpR) mediating resistance against the antibiotic ampicillin. The gene of the 198/B1 (clone AB2)-scFv was rescued from plasmid pDAP2-198AB2#100 (example 16) by digestion with SfiI and NotI and inserted into SfiI/NotI cleaved pMycHis6. The resultant plasmid was designated pMycHis-198AB2#102. Fig. 34 shows the nucleotide and amino acid sequence of 198AB2 scFv (linked to the c-myc-tag and the His6-tag):the resulting ORF of the expression vector is named pMycHis6-198AB2#102. Vector pMycHis6 was constructed by cleaving vector pCOCK (Engelhardt O. et al, BioTechniques 17, 44-46, 1994) NotI - EcoRI and inserting the following annealed oligonucleotides: (5'-GGCCGCAGAACAACAAAACTCATCTCAGAAGAGGATCTGAATGGG GCGGCACATCACCATCACCATCACTAATAAG - 3' (SEQ.ID.No. 103) and 5'-TTATTAGTGATGGTGTATGGT GATGTGCCGCCCCATTGAGATCCTCTTCTGAGATGAGTTTTTGTCTCTGC-3'(SEQ.ID.NO. 104)). The resultant vector, named pMycHis6, was cleaved SfiI - NotI and the gene of scFv 198AB2 was swapped into this vector from vector pDAP2-198AB2#100. In analogy to the 198AB2 construct, the #8860 scFv fragment was cloned from a plasmid designated pDAP2-8860scFv clone 11. The pure scFv protein of #8860 was designated 8860-M/H#4c (plasmid p8860-M/H#4c, Fig. 35). The scFv proteins were expressed in E. coli and affinity purified from bacterial supernatants on Protein L columns (see example 17). The final MycHis-198AB2#102 and 8860-M/H#4c preparations were dialyzed against 50mM imidazole, 100mM NaCl, pH7.4 and analyzed in a chromogenic FVIII assay as described above (Fig. 36).

[0116] As can be seen in Fig. 36, the scFv construct MycHis-198AB2#102 gave rise to a substantial FXa generation whereas the negative controls 8860-M/H#4c and plain reaction buffer (IZ) did not. Fig. 36 demonstrates the chromogenic FVIII-like activity of the 198/B1 (subclone AB2) scFv fragment (MycHis-198AB2#102) in the presence of 2.3nM human FIXa. As a positive control we used 4.8pM FVIII whereas a unrelated scFv (8860-M/H#4c) and plain reaction buffer (IZ) served as negative controls.

SEQUENZPROTOKOLL

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10     gctgatgact tcaagggacg gtttgccctc tctttggaaa cctctgccag cactgcctat 240
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      ggaggcgggt caggtgggcg cgcctctggc ggtggcggat cggatattca gatgacacag 420
      tctcccaaat tcctgcttgt atcagcagga gacagggtta ccataacctg caaggccagt 480
15     cagagtgtga gtaatgatgt agcttggtac caacagaagc cggggcagtc tcctaaacta 540
      ctgatgtact atgcatccaa tcgctacact ggagtccttg atcgcttcac tggcagtgga 600
      tatgggacgg atttcacttt caccatcagc actgtgcagg ctgaagacct ggcagtttat 660

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      ttctgtcagc aggattatgg ctctcctccc acgttcggag ggggcaccaa gctggaaatt 720
25     aaacgg                                     726

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<210> 82

<211> 242

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<212> PRT

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:scFv region

35

<400> 82

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55

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	1				5					10					15		
5	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Thr	Asn	Tyr	
				20					25					30			
	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp	Met	
10			35					40					45				
	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Asp	Asp	Phe	
		50					55					60					
15	Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Ser	Thr	Ala	Tyr	
	65					70					75					80	
	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Asn	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	
20					85					90					95		
	Ala	Leu	Tyr	Gly	Asn	Ser	Pro	Lys	Gly	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	
25				100					105					110			
	Thr	Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Arg	Ala	
			115					120					125				
30	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Lys	Phe	
	130						135					140					
	Leu	Leu	Val	Ser	Ala	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	
35	145					150					155					160	
	Gln	Ser	Val	Ser	Asn	Asp	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
40					165					170					175		
	Ser	Pro	Lys	Leu	Leu	Met	Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	
				180					185					190			

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Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr
195 200 205

5 Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
210 215 220

10 Asp Tyr Gly Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Arg

15
<210> 83
<211> 747
<212> DNA
<213> Künstliche Sequenz

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<220>
<223> Beschreibung der kunstlichen Sequenz:scFv region

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<400> 83

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ggacacgggt acggtagtag ctttgactac tggggccaag gcaccactct cacagtctcc 360
tcaggtggag gcggttcagg tgggcgcgcc tctggcggtg gcggatcgca aattgtgctc 420
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ggaggcacca agctggaaat caaacgg 747

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<210> 84
<211> 249
<212> PRT
<213> Künstliche Sequenz

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<220>
<223> Beschreibung der kunstlichen Sequenz:scFv region

<400> 84

55 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

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5	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Thr	Tyr
				20					25					30		
	Thr	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Glu	Lys	Arg	Leu	Glu	Trp	Val
10			35					40					45			
	Ala	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Tyr	Thr	Tyr	Tyr	Pro	Asp	Ser	Val
		50					55					60				
15	Arg	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
	65					70				75					80	
	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
20					85				90					95		
	Thr	Arg	Asp	Gly	Gly	His	Gly	Tyr	Gly	Ser	Ser	Phe	Asp	Tyr	Trp	Gly
				100					105					110		
25	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
			115					120					125			
	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro
30		130					135					140				
	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg
35		145				150				155					160	
	Ser	Ser	Gln	Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp
				165					170					175		
40	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val
			180					185						190		
	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Lys	Phe	Ser	Gly	Ser	Gly	Ser
45			195					200					205			
	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu
		210					215					220				
50	Gly	Val	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Trp	Thr	Phe	Gly
	225				230					235					240	
	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg							
55				245												

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<210> 85
 <211> 747
 <212> DNA
 <213> Künstliche Sequenz

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<220>
 <223> Beschreibung der künstlichen Sequenz:scFv region

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<400> 85

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ctgcaaatga gcagtctgag gtctgaggac acagccatgt attactgtac aagagagggg 300
ggtggtttca ccgtcaactg gtacttcgat gtctggggcg cagggactct ggtcactgtc 360
tctgcagggtg gaggcggttc aggtgggcgc gcctctggcg gtggcggatc ggaaaatgtg 420
ctcaccacgt ctccagcttc tttggctgtg tctctagggc agagggccac catatcctgc 480
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gccaggttca gtggcagtgg gtctaggaca gacttcaccc tcaccattaa tctgtggag 660
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<210> 86
 <211> 249
 <212> PRT
 <213> Künstliche Sequenz

35

<220>
 <223> Beschreibung der künstlichen Sequenz:scFv region

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<400> 86

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Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 5 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 10 Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45
 15 Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 20
 25
 30
 35
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 45
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5 Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Thr Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp
 100 105 110
 10 Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly
 115 120 125
 Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser
 15 130 135 140
 Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 145 150 155 160
 20 Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp
 165 170 175
 25 Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
 180 185 190
 Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 30 195 200 205
 Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
 210 215 220
 35 Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
 225 230 235 240
 40 Thr Gly Thr Arg Leu Glu Ile Lys Arg
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45 <210> 87
 <211> 747
 <212> DNA
 <213> Künstliche Sequenz
 <220>
 50 <223> Beschreibung der künstlichen Sequenz:scFv region
 <400> 87

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 ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atcactgtac aagagagggg 300

10 ggtggttatt acgtcaactg gtacttcgat gtctggggcg caggcaccac tctcacagtc 360
 tcctcaggtg gaggcggttc aggtggggcg gcctctggcg gtggcggatc ggacattgag 420
 ctacncagt ctccagcttc tttggctgtg tctctagggc agagggccac catatcctgc 480
 15 agagccagtg aaagtgttga tagttatggc aagagtttta tgcactggta ccagcagaaa 540
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 gccaggttca gtggcagtgg gtctaggaca gacttcaccc tcaccattaa tcctgtggag 660
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 20 gctgggacca gactggaaat aaaacggg 747

<210> 88
 <211> 249
 25 <212> PRT
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der kunstlichen Sequenz:scFv region
 30 <400> 88

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 1 5 10 15
 5 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
 20 25 30
 10 Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45
 Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
 50 55 60
 15 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 20 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys
 85 90 95
 25 Thr Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp
 100 105 110
 Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 30 Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
 130 135 140
 35 Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 145 150 155 160

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Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp
 165 170 175
 5
 Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
 180 185 190
 10
 Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 195 200 205
 15
 Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
 210 215 220
 Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
 225 230 235 240
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 Ala Gly Thr Arg Leu Glu Ile Lys Arg
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 <210> 89
 <211> 2199
 <212> DNA
 <213> Künstliche Sequenz
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 <220>
 <223> Beschreibung der kunstlichen Sequenz:scFv region
 35
 <400> 89

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 5 aaactctcct gtgcagcctc tggattcact ttcagtagct ataccatgtc ttgggttcgc 180
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 tcctgcagag ccagtgaag tgttgatagt tatggctata attttatgca ctggtatcag 600
 15 cagataccag gacagccacc caaactctc atctatcgtg catccaacct agagtctggg 660
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 35 ggcggcggcg caaaaacctt tgctgaaacg gcaaccgctg gtgaatggca gggaaaaacg 1500
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<210> 90

<211> 732

55 <212> PRT

<213> Künstliche Sequenz

<220>

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<223> Beschreibung der künstlichen Sequenz:scFv region

<400> 90

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10     Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
              20              25              30

15     Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
              35              40              45

      Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
              50              55              60

20     Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
      65              70              75              80

25     Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
              85              90              95

      Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp

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10	Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser 130 135 140		
	Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp 145 150 155 160		
15	Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln 165 170 175		
20	Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly 180 185 190		
	Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys 195 200 205		
25	Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg 210 215 220		
30	Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro 225 230 235 240		
	Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu 245 250 255		
35	Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala 260 265 270		
40	Ala Ala Ala Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala 275 280 285		
	Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp 290 295 300		
45	Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn 305 310 315 320		
50	Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala 325 330 335		
	Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp 340 345 350		
55	Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys		

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	355	360	365
5	Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala 370	375	380
10	Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile 385	390	395 400
	His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly 405	410	415
15	Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro 420	425	430
20	Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser 435	440	445
	Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys 450	455	460
25	Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu 465	470	475 480
30	Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp 485	490	495
	Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu 500	505	510
35	Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln 515	520	525
40	Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp 530	535	540
	Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val 545	550	555 560
45	Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala 565	570	575
50	Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly 580	585	590
	Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala 595	600	605
55	Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala		

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	610	615	620
5	Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val		
	625	630	635 640
10	Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp		
		645	650 655
15	Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala		
		660	665 670
20	Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His		
		675	680 685
25	Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn		
		690	695 700
30	Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala		
		705	710 715 720
35	Ala Leu Gly Asp Ile Ala His His His His His His		
		725	730

<210> 91

<211> 978

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:scFv region

<400> 91

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 5 aaactctcct gtgcagcctc tggattcact ttcagtagct ataccatgtc ttgggttcgc 180
 cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggnng tagttccacc 240
 tactatccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc 300
 ctgtacctgc aaatgagcag tctgaggtct gaggacacag ccatgtatta ctgtacaaga 360
 gaggggggtg gtttcaccgt caactgggtac ttcgatgtct ggggcgcagg aacctcagtc 420
 10 accgtctcct caggtggagg cggttcaggt gggcgcgcct ctggcgggtg cggatcggac 480
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 <212> PRT
 <213> Künstliche Sequenz

35 <220>
 <223> Beschreibung der künstlichen Sequenz:scFv region
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5	Ala	Gln	Pro	Ala	Met	Ala	Glu	Val	Lys	Leu	Val	Glu	Ser	Gly	Gly	Gly
				20					25					30		
	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly
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	Lys	Arg	Leu	Glu	Trp	Val	Ala	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Ser	Thr
	65					70					75					80
20	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn
					85					90					95	
	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Arg	Ser	Glu	Asp
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	Thr	Ala	Met	Tyr	Tyr	Cys	Thr	Arg	Glu	Gly	Gly	Gly	Phe	Thr	Val	Asn
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	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser
	130						135						140			
35	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Asp
	145					150					155					160
	Ile	Val	Leu	Thr	Gln	Xaa	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln
40					165					170					175	
	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	Ser	Val	Asp	Ser	Tyr	Gly
45				180					185					190		

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Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
 195 200 205
 5
 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
 210 215 220
 10
 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
 225 230 235 240
 15
 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
 245 250 255
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
 260 265 270
 20
 Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln
 275 280 285
 25
 Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu
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 His His His His His
 325
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<210> 93

<211> 2190

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:scFv region

<400> 93

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<210> 94
 <211> 729
 <212> PRT
 <213> Künstliche Sequenz

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<220>

<223> Beschreibung der künstlichen Sequenz:scFv region

<400> 94

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Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
20 25 30

15

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
35 40 45

20

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly

25

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35

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5	Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr					
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	Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys					
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	Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp					
		100		105		110
15	Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met					
		115		120		125
	Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly					
20		130		135		140
	Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu					
	145		150		155	160
25	Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr					
		165		170		175
	Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr					
30		180		185		190
	Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile					
		195		200		205
35	Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly					
		210		215		220
	Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu					
40		225		230		235
	Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg					
		245		250		255
45	Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ala					
		260		265		270
	Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp					
50		275		280		285
	Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala					
		290		295		300
55	Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu					

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	305		310		315		320
5	Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn	325		330		335	
	Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro	340		345		350	
10	Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys	355		360		365	
	Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr	370		375		380	
15	Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys	385		390		395	400
20	Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr	405		410		415	
	Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu	420		425		430	
25	Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser	435		440		445	
30	Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile	450		455		460	
	Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly	465		470		475	480
	Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys	485		490		495	
40	Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp	500		505		510	
	Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu	515		520		525	
45	Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro	530		535		540	
50	Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr	545		550		555	560
55	Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr						

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					565					570					575	
5	Asp	Lys	Ala	Ile	Glu	Leu	Leu	Ser	Lys	Asn	Glu	Lys	Gly	Phe	Phe	Leu
					580				585					590		
	Gln	Val	Glu	Gly	Ala	Ser	Ile	Asp	Lys	Gln	Asp	His	Ala	Ala	Asn	Pro
10			595					600					605			
	Cys	Gly	Gln	Ile	Gly	Glu	Thr	Val	Asp	Leu	Asp	Glu	Ala	Val	Gln	Arg
		610					615					620				
15	Ala	Leu	Glu	Phe	Ala	Lys	Lys	Glu	Gly	Asn	Thr	Leu	Val	Ile	Val	Thr
	625					630					635					640
20	Ala	Asp	His	Ala	His	Ala	Ser	Gln	Ile	Val	Ala	Pro	Asp	Thr	Lys	Ala
					645					650					655	
	Pro	Gly	Leu	Thr	Gln	Ala	Leu	Asn	Thr	Lys	Asp	Gly	Ala	Val	Met	Val
25					660				665					670		
	Met	Ser	Tyr	Gly	Asn	Ser	Glu	Glu	Asp	Ser	Gln	Glu	His	Thr	Gly	Ser
			675					680					685			
30	Gln	Leu	Arg	Ile	Ala	Ala	Tyr	Gly	Pro	His	Ala	Ala	Asn	Val	Val	Gly
		690					695					700				
35	Leu	Thr	Asp	Gln	Thr	Asp	Leu	Phe	Tyr	Thr	Met	Lys	Ala	Ala	Leu	Gly
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<210> 95

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<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:scFv region

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<400> 95

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cagaggcctg gacagggctc tgagtggatt ggacggattt atcctggaaa tggagatact 240
aactacaatg ggaagttcaa gggcaaggcc aactgactg cagacaaatc ctccagcaca 300
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gccagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaacca 600
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<210> 96
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<212> PRT
<213> Künstliche Sequenz

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<220>
<223> Beschreibung der künstlichen Sequenz:scFv region

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<400> 96

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5 Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
20 25 30

10 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
35 40 45

15 Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
65 70 75 80

20 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
85 90 95

25 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
100 105 110

30 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
130 135 140

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5 Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu
 145 150 155 160
 Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
 165 170 175
 10 Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 180 185 190
 15 Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 195 200 205
 Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 210 215 220
 20 Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
 225 230 235 240
 25 Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
 245 250 255
 30 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro
 260 265 270
 Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp
 275 280 285
 35 Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val
 290 295 300
 40 Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His His
 305 310 315 320
 45 His His

<210> 97

<211> 270

<212> DNA

<213> Künstliche Sequenz

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<223> Beschreibung der künstlichen Sequenz:scFv region

<400> 97

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agccggccat ggcccagggtg cagctgcagg cgcgcctgca ggtcgacctc gagatcaaac 180
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<210> 98

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<211> 61

<212> PRT

<213> Künstliche Sequenz

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<223> Beschreibung der künstlichen Sequenz:scFv region

<400> 98

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu Gln Val
20 25 30

Asp Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu
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Glu Asp Leu Asn Gly Ala Ala His His His His His His
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<210> 99

<211> 888

<212> DNA

<213> Künstliche Sequenz

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<220>

<223> Beschreibung der künstlichen Sequenz:scFv region

<400> 99

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 20 gtggaggctg atgatgttgc aacctattac tgtcagcaaa gtaatgagga tccgctcacg 780
 ttcggtactg ggaccagact ggaaataaaa cgggcggccg cagaacaaaa actcatctca 840
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<210> 100

<211> 294

<212> PRT

30 <213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:scFv region

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<400> 100

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	1				5						10					15
5	Ala	Gln	Pro	Ala	Met	Ala	Glu	Val	Lys	Leu	Val	Glu	Ser	Gly	Gly	Gly
				20					25					30		
10	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly
			35					40					45			
15	Phe	Thr	Phe	Ser	Ser	Tyr	Thr	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Glu
		50					55					60				
20	Lys	Arg	Leu	Glu	Trp	Val	Ala	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Ser	Thr
	65					70					75					80
25	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn
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30	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Arg	Ser	Glu	Asp
				100					105					110		
35	Thr	Ala	Met	Tyr	Tyr	Cys	Thr	Arg	Glu	Gly	Gly	Gly	Gly	Phe	Thr	Val
			115					120						125		
40	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser
		130					135					140				
45	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Asp
	145					150					155					160
50	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln
					165					170					175	
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 180 185 190
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 Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
 195 200 205
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 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
 210 215 220
 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
 15 225 230 235 240
 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
 20 245 250 255
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
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 Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 275 280 285
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 <210> 101
 <211> 876
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 <213> Künstliche Sequenz
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 <223> Beschreibung der kunstlichen Sequenz:scFv region
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 5 cagaggcctg gacagggctc tgagtggatt ggacggattt atcctggaaa tggagatact 240
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 gcctacatgc agctcagcag cctgacctct gtggactctg cggctctattt ctgtgcagat 360
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	1				5					10					15		
5	Ala	Gln	Pro	Ala	Met	Ala	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	
				20					25					30			
10	Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
			35					40					45				
15	Tyr	Ala	Phe	Ser	Ser	Ser	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	
		50					55					60					
20	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Arg	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	
	65					70					75					80	
25	Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	
					85					90					95		
30	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Val	Asp	
				100				105						110			
35	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Asp	Gly	Asn	Val	Tyr	Tyr	Tyr	Ala	Met	
			115					120					125				
40	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	
		130					135					140					
45	Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ile	Val	Leu	
	145					150					155					160	
50	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	
					165					170					175		
55	Ile	Ser	Cys	Arg	Ala	Ser	Lys	Ser	Val	Ser	Thr	Ser	Gly	Tyr	Ser	Tyr	
				180					185					190			

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Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
195 200 205

5

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
210 215 220

10

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
225 230 235 240

15

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
245 250 255

20

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu
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35

40

Claims

1. An antibody against factor IX/factor IXa which has a factor VIIIa-cofactor activity and increases the procoagulant activity of FIXa.
2. The antibody according to claim 1, wherein said antibody increases the procoagulant activity of FIXa in the presence of FVIII inhibitors.
3. The antibody according to claim 1 or 2, wherein said antibody is selected from the group consisting of IgG, IgM, IgA and IgE antibodies.
4. The antibody according to claim 1, wherein said antibody is selected from the group consisting of monoclonal antibodies, chimeric antibodies, humanized antibodies, single chain antibodies, bispecific antibodies, diabodies, scFv, Fab, F(ab)₂, and di-, oligo- or multimers thereof.
5. The antibody according to anyone of claims 1 to 4, wherein the complement determining region (CDR) peptide is a CDR3 peptide comprising an amino acid sequence selected from the group consisting of:

55

Tyr-Gly-Asn-Ser-Pro-Lys-Gly-Phe-Ala-Tyr and
Asp-Gly-Gly-His-Gly-Tyr-Gly-Ser-Ser-Phe-Asp-Tyr.

- 5 6. The antibody according to anyone of claims 1 to 5, wherein the nucleotide sequence encoding the variable region of said antibody comprises nucleotides 1 to 357 and nucleotides 403 to 726 according to Fig. 14.
7. The antibody according to claim 6, wherein said antibody additionally comprises an artificial linker sequence.
- 10 8. The antibody according to anyone of claims 1 to 5, wherein the nucleotide sequence encoding the variable region of said antibody comprises nucleotides 1 to 363 and nucleotides 409 to 747 according to Fig. 15.
9. The antibody according to claim 8, wherein said antibody additionally comprises an artificial linker sequence.
- 15 10. The antibody according to anyone of claims 1 to 5, wherein the nucleotide sequence encoding the variable region of said antibody comprises nucleotides 1 to 366 and nucleotides 412 to 747 according to Fig. 16.
11. The antibody according to claim 10, wherein said antibody additionally comprises an artificial linker sequence.
- 20 12. A hybridoma cell line expressing an antibody against factor IX/factor IXa according to anyone of claims 1 to 11.
13. The hybridoma cell line according to claim 12, wherein said cell line is selected from the group consisting of 198/B1 ECACC No. 99090925; 198/A1 ECACC No. 99090924; 198/BB1 ECACC No. 99090926; 193/A0 ECACC No. 99121614; 196/C4 ECACC No. 99121615; 198/D1 ECACC No. 99121616; 198/T2 ECACC No. 99121617; 198/G2 ECACC No. 99121618; 198/AC1 ECACC No. 99121619; 198/U2 ECACC No. 99121620.
- 25 14. The antibody according to anyone of claims 1 to 11, which is expressed by a hybridoma cell line according to claim 12 or 13.
- 30 15. A DNA molecule, wherein said DNA molecule encodes an antibody according to anyone of claims 1 to 11.
16. A pharmaceutical preparation comprising an antibody according to anyone of claims 1 to 11 and a pharmaceutically acceptable carrier.
- 35 17. The preparation according to claim 16, additionally comprising factor IXa α and/or factor IXa β .
18. A method for obtaining an antibody according to claim 1 comprising the steps of:
 - immunizing a non human mammal with an antigen selected from the group consisting of factor IX, factor IXa α , factor IXa β or fragments thereof;
 - 40 - isolating spleen cells of the immunized mammal;
 - producing hybridoma clones;
 - screening the hybridoma cell supernatants for an increase in the procoagulant activity of factor IXa;
 - isolating the hybridoma clones expressing the antibodies; and
 - 45 - isolating the antibodies.
19. Use of an antibody according to anyone of claims 1 and 2 in the manufacture of a medicament for the treatment of a blood coagulation disorder in a patient.
- 50 20. Use according to claim 19, wherein the blood coagulation disorder is selected from the group consisting of hemophilia A and hemorrhagic diathesis.
21. Use according to claims 19 or 20, wherein the patients are hemophilia inhibitor patients.

55 Patentansprüche

1. Antikörper gegen Faktor IX/Faktor IXa, der eine Faktor VIIIa-Kofaktor-Aktivität aufweist und die prokoagulierende Aktivität von FIXa erhöht.

2. Antikörper nach Anspruch 1, wobei der Antikörper die prokoagulierende Aktivität von FIXa in der Anwesenheit von FVIII-Inhibitoren erhöht.
- 5 3. Antikörper nach Anspruch 1 oder 2, wobei der Antikörper ausgewählt ist aus der Gruppe, bestehend aus IgG-, IgM-, IgA- und IgE-Antikörpern.
- 10 4. Antikörper nach Anspruch 1, wobei der Antikörper ausgewählt ist aus der Gruppe, bestehend aus monoklonalen Antikörpern, chimären Antikörpern, humanisierten Antikörpern, Einzelkettenantikörpern, bispezifischen Antikörpern, Diabodies, scFv, Fab, F(ab)₂, und Di-, Oligo- oder Multimeren davon.
- 15 5. Antikörper nach einem der Ansprüche 1 bis 4, wobei das komplementäritätsbestimmende Region (CDR)-Peptid ein CDR3-Peptid ist, umfassend eine Aminosäuresequenz, ausgewählt aus der Gruppe bestehend aus:

Tyr-Gly-Asn-Ser-Pro-Lys-Gly-Phe-Ala-Tyr und
Asp-Gly-Gly-His-Gly-Tyr-Gly-Ser-Ser-Phe-Asp-Tyr.
- 20 6. Antikörper nach einem der Ansprüche 1 bis 5, wobei die Nukleotidsequenz, welche die variable Region des Antikörpers kodiert, die Nukleotide 1 bis 357 und die Nukleotide 403 bis 726 nach Fig. 14 umfaßt.
- 25 7. Antikörper nach Anspruch 6, wobei der Antikörper zusätzlich eine künstliche Verbindungs (Linker)-Sequenz umfaßt.
8. Antikörper nach einem der Ansprüche 1 bis 5, wobei die Nukleotidsequenz, welche die variable Region des Antikörpers kodiert, die Nukleotide 1 bis 363 und die Nukleotide 409 bis 747 nach Fig. 15 umfaßt.
- 30 9. Antikörper nach Anspruch 8, wobei der Antikörper zusätzlich eine künstliche Verbindungs (Linker)-Sequenz umfaßt.
10. Antikörper nach einem der Ansprüche 1 bis 5, wobei die Nukleotidsequenz, welche die variable Region des Antikörpers kodiert, die Nukleotide 1 bis 366 und die Nukleotide 412 bis 747 nach Fig. 16 umfaßt.
- 35 11. Antikörper nach Anspruch 10, wobei der Antikörper zusätzlich eine künstliche Verbindungs (Linker)-Sequenz umfaßt.
12. Hybridomazelllinie, welche einen Antikörper gegen Faktor IX/Faktor IXa nach einem der Ansprüche 1 bis 11 exprimiert.
- 40 13. Hybridomazelllinie nach Anspruch 12, wobei die Zelllinie ausgewählt ist aus der Gruppe, bestehend aus 198/B1 ECACC Nr. 99090925; 198/A1 ECACC Nr. 99090924; 198/BB1 ECACC Nr. 99090926; 193/A0 ECACC Nr. 99121614; 196/C4 ECACC Nr. 99121615; 198/D1 ECACC Nr. 99121616; 198/T2 ECACC Nr. 99121617; 198/G2 ECACC Nr. 99121618; 198/AC1 ECACC Nr. 99121619; 198/U2 ECACC Nr. 99121620.
- 45 14. Antikörper nach einem der Ansprüche 1 bis 11, der von einer Hybridomazelllinie nach Anspruch 12 oder 13 exprimiert ist.
15. DNA-Molekül, wobei das DNA-Molekül einen Antikörper nach einem der Ansprüche 1 bis 11 kodiert.
- 50 16. Pharmazeutische Zusammensetzung, umfassend einen Antikörper nach einem der Ansprüche 1 bis 11 und einen pharmazeutisch verträglichen Träger.
17. Zusammensetzung nach Anspruch 16, zusätzlich umfassend Faktor IXa α und/oder Faktor IXa β .
- 55 18. Verfahren zum Erhalten eines Antikörpers nach Anspruch 1, umfassend die Schritte:
 - Immunisieren eines nicht-menschlichen Säugetiers mit einem Antigen, ausgewählt aus der Gruppe, bestehend aus Faktor IX, Faktor IXa α , Faktor IXa β oder Fragmenten davon;
 - Isolieren von Milzzellen des immunisierten Säugetiers;
 - Herstellen von Hybridomaklonen;
 - Screenen der Hybridomazellüberstände nach einem Anstieg der prokoagulierenden Aktivität von Faktor IXa;
 - Isolieren der Hybridomaklone, welche die Antikörper exprimieren; und
 - Isolieren der Antikörper.

19. Verwendung eines Antikörpers nach einem der Ansprüche 1 und 2 in der Herstellung eines Arzneimittels zur Behandlung einer Blutgerinnungsstörung in einem Patienten.
20. Verwendung nach Anspruch 19, wobei die Blutgerinnungsstörung ausgewählt ist aus der Gruppe, bestehend aus Hämophilie A und hämorrhagischer Diathese.
21. Verwendung nach einem der Ansprüche 19 oder 20, wobei die Patienten Hämophilie-Inhibitor-Patienten sind.

Revendications

1. Anticorps contre le facteur IX/facteur IXa qui possède une activité de cofacteur du facteur VIIIa et augmente l'activité pro-coagulante du FIXa.
2. Anticorps selon la revendication 1, dans lequel ledit anticorps augmente l'activité pro-coagulante du FIXa en présence d'inhibiteurs du FVIII.
3. Anticorps selon la revendication 1 ou 2, dans lequel ledit anticorps est choisi dans le groupe constitué par des anticorps d'IgG, d'IgM, d'IgA et d'IgE.
4. Anticorps selon la revendication 1, dans lequel ledit anticorps est choisi dans le groupe constitué par des anticorps monoclonaux, des anticorps chimères, des anticorps humanisés, des anticorps monocaténaux, des anticorps bispécifiques, des diacorps, scFv, Fab, F(ab)₂, et des di-, oligo- ou multimères de ceux-ci.
5. Anticorps selon l'une quelconque des revendications 1 à 4, dans lequel le peptide de la région hypervariable ("complement determining region peptide" en langue anglaise) (CDR), est un peptide CDR3 comprenant une séquence d'acides aminés choisie dans le groupe constitué par :

Tyr-Gly-Asn-Ser-Pro-Lys-Gly-Phe-Ala-Tyr et
Asp-Gly-Gly-His-Gly-Tyr-Gly-Ser-Ser-Phe-Asp-Tyr.
6. Anticorps selon l'une quelconque des revendications 1 à 5, dans lequel la séquence nucléotidique codant la région variable dudit anticorps comprend les nucléotides 1 à 357 et les nucléotides 403 à 726 selon la Fig. 14.
7. Anticorps selon la revendication 6, dans lequel ledit anticorps comprend de plus une séquence de liaison artificielle.
8. Anticorps selon l'une quelconque des revendications 1 à 5, dans lequel la séquence nucléotidique codant la région variable dudit anticorps comprend les nucléotides 1 à 363 et les nucléotides 409 à 747 selon la Fig. 15.
9. Anticorps selon la revendication 8, dans lequel ledit anticorps comprend de plus une séquence de liaison artificielle.
10. Anticorps selon l'une quelconque des revendications 1 à 5, dans lequel la séquence nucléotidique codant la région variable dudit anticorps comprend les nucléotides 1 à 366 et les nucléotides 412 à 747 selon la Fig. 16.
11. Anticorps selon la revendication 10, dans lequel ledit anticorps comprend de plus une séquence de liaison artificielle.
12. Lignée cellulaire d'hybridome exprimant un anticorps contre le facteur IX/facteur IXa selon l'une quelconque des revendications 1 à 11.
13. Lignée cellulaire d'hybridome selon la revendication 12, dans laquelle ladite lignée cellulaire est choisie dans le groupe constitué par 198/B 1 ECACC No. 99090925 ; 198/A1 ECACC. No. 99090924 ; 198/BB1 ECACC No. 99090926 ; 193/A0 ECACC No. 99121614 ; 196/C4 ECACC No. 99121615 ; 198/D1 ECACC No. 99121616 ; 198/T2 ECACC No. 99121617 ; 198/G2 ECACC No. 99121618 ; 198/AC1 ECACC No. 99121619 ; 198/U2 ECACC No. 99121620.
14. Anticorps selon l'une quelconque des revendications 1 à 11, qui est exprimé par une lignée cellulaire d'hybridome selon la revendication 12 ou 13.

15. Molécule d'ADN, dans laquelle ladite molécule d'ADN code un anticorps selon l'une quelconque des revendications 1 à 11.

16. Préparation pharmaceutique comprenant un anticorps selon l'une quelconque des revendications 1 à 11 et un véhicule acceptable du point de vue pharmaceutique.

17. Préparation selon la revendication 16, comprenant de plus le facteur IXa α et/ou le facteur IXa β .

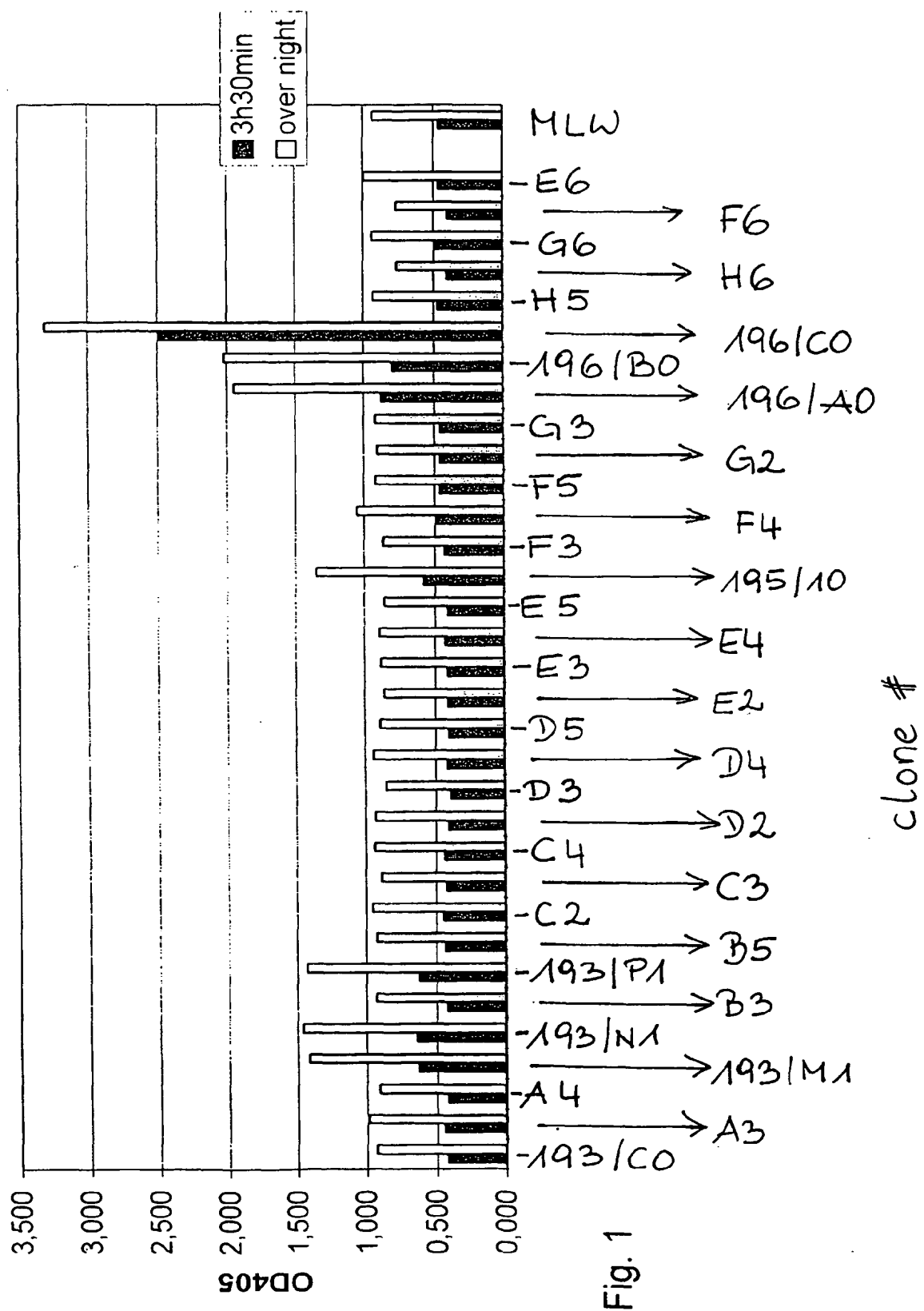
18. Procédé d'obtention d'un anticorps selon la revendication 1 comprenant les étapes :

- d'immunisation d'un mammifère non humain avec un antigène choisi dans le groupe constitué par le facteur IX, le facteur IXa α , le facteur IXa β ou des fragments de ceux-ci ;
- d'isolement des cellules de la rate du mammifère immunisé ;
- de production de clones d'hybridome ;
- de sélection des surnageants cellulaires de l'hybridome présentant une augmentation de l'activité pro-coagulante du facteur IXa ;
- d'isolement des clones de l'hybridome exprimant les anticorps ; et
- d'isolement des anticorps.

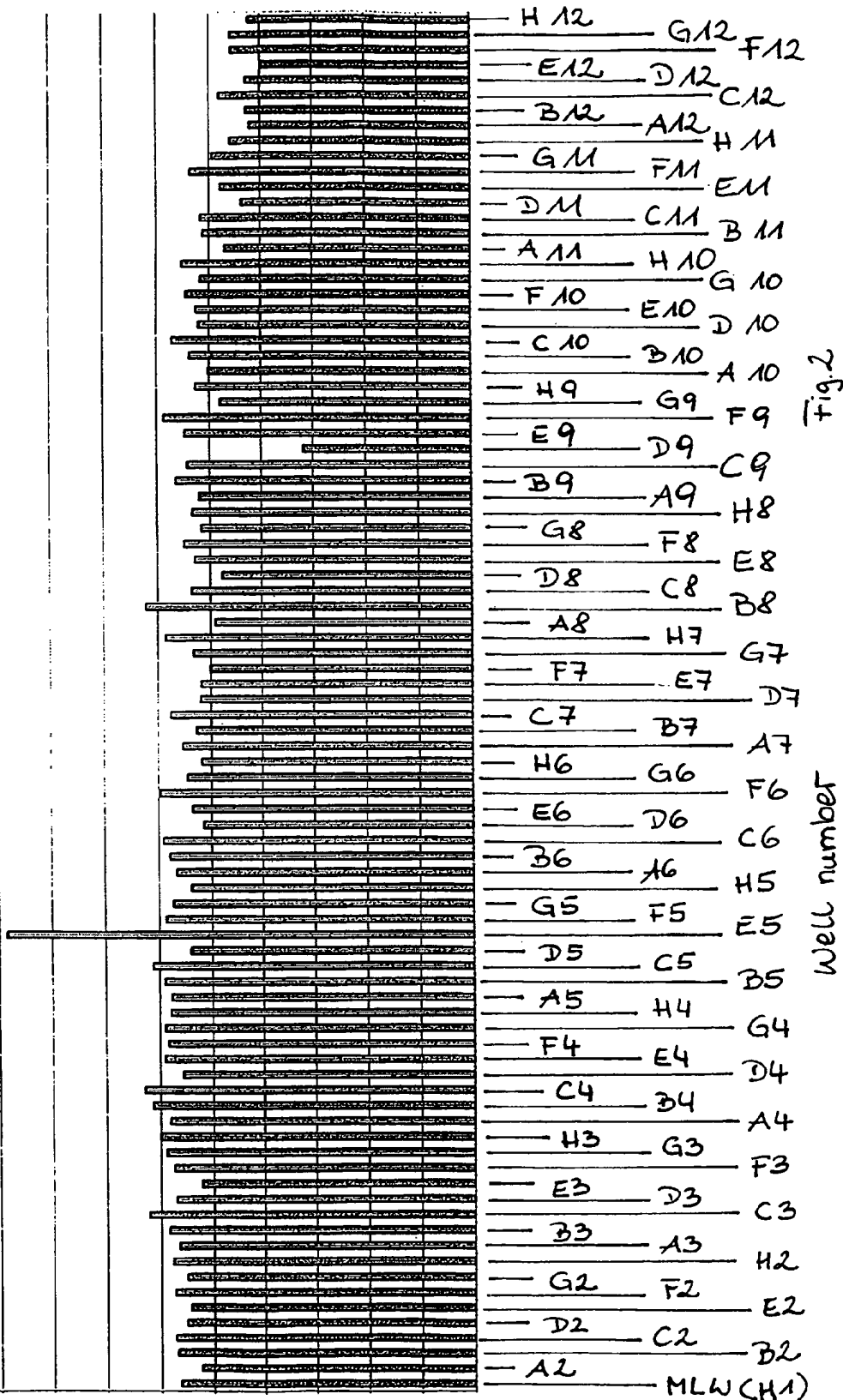
19. Utilisation d'un anticorps selon l'une quelconque des revendications 1 et 2 pour la fabrication d'un médicament pour le traitement d'un trouble de la coagulation sanguine chez un patient.

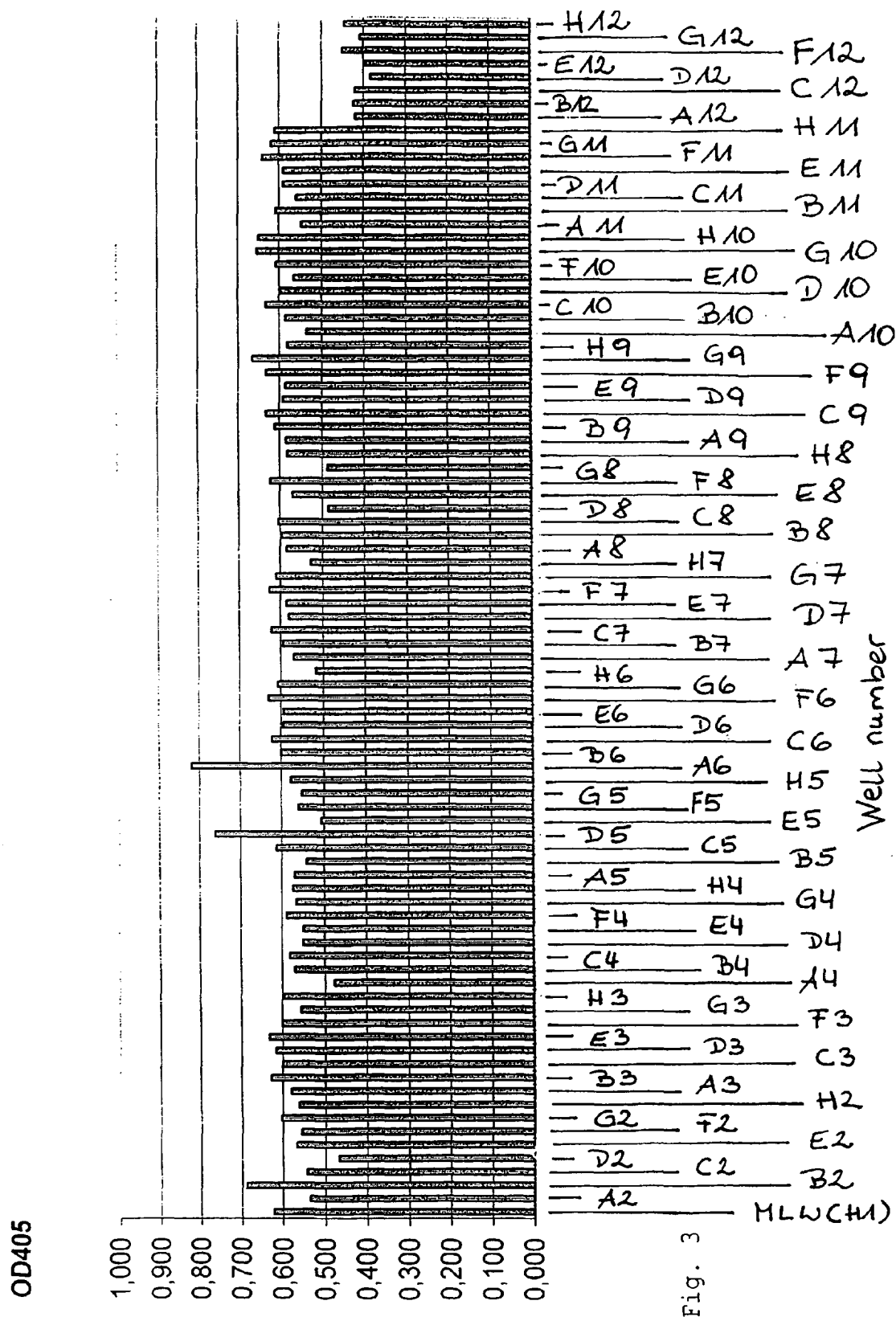
20. Utilisation selon la revendication 19, dans laquelle le trouble de la coagulation sanguine est choisi dans le groupe constitué par l'hémophilie A et la diathèse hémorragique.

21. Utilisation selon les revendications 19 ou 20, dans laquelle les patients sont des patients inhibiteurs d'hémophilie.



OD405





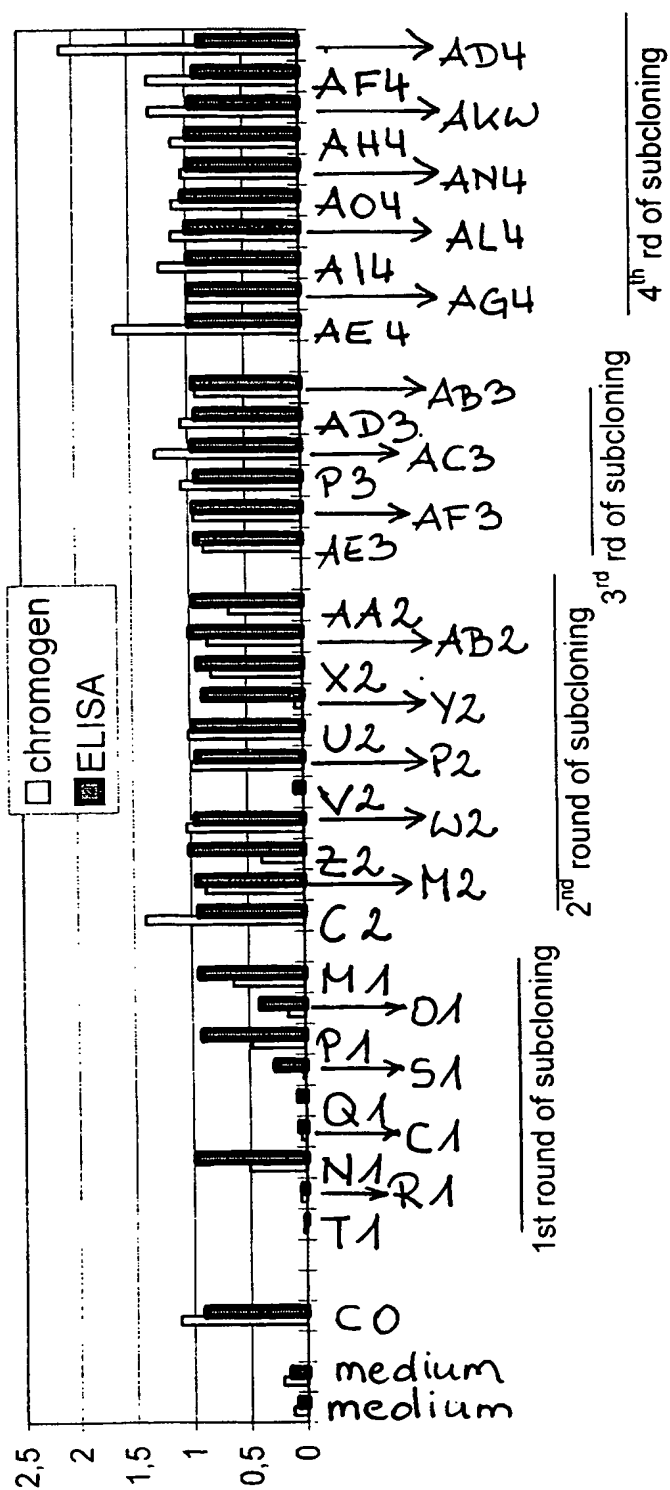


Fig. 4

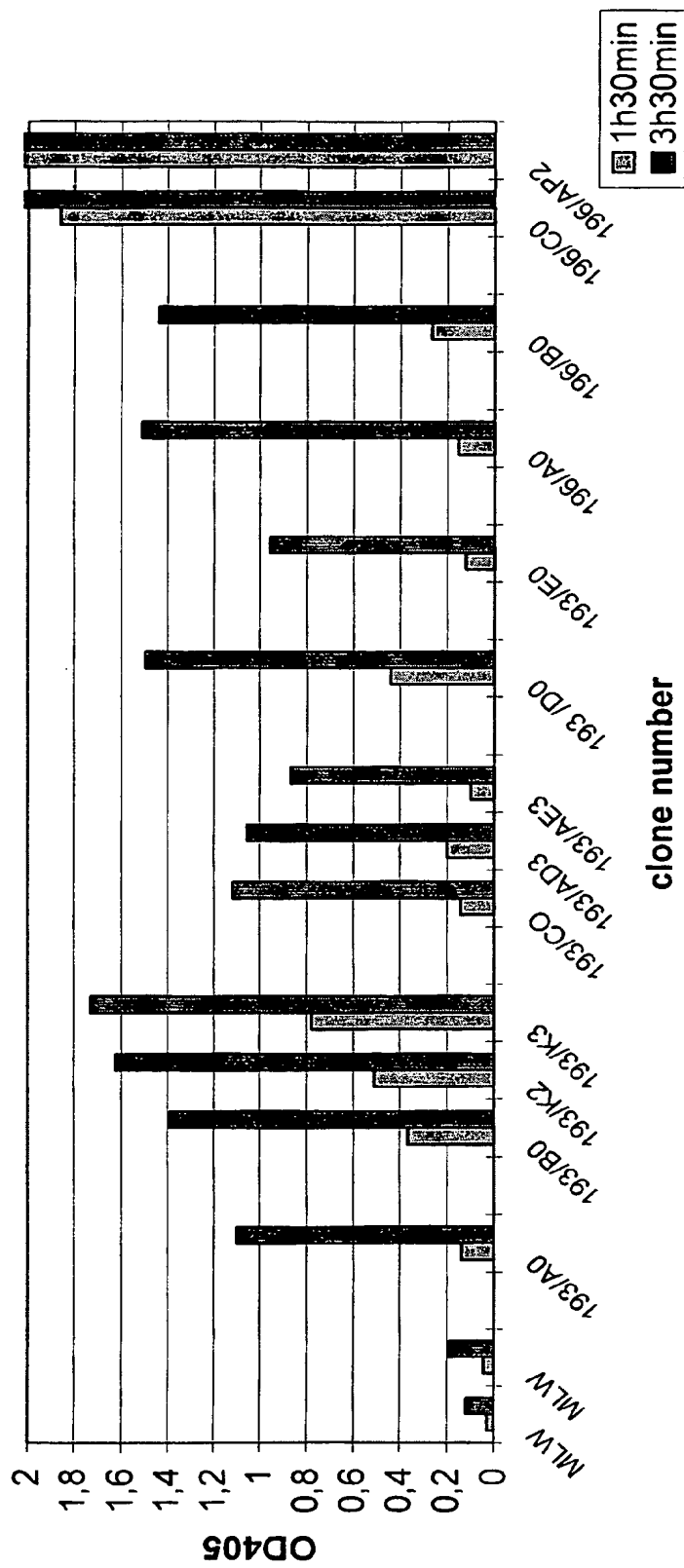


Fig. 5

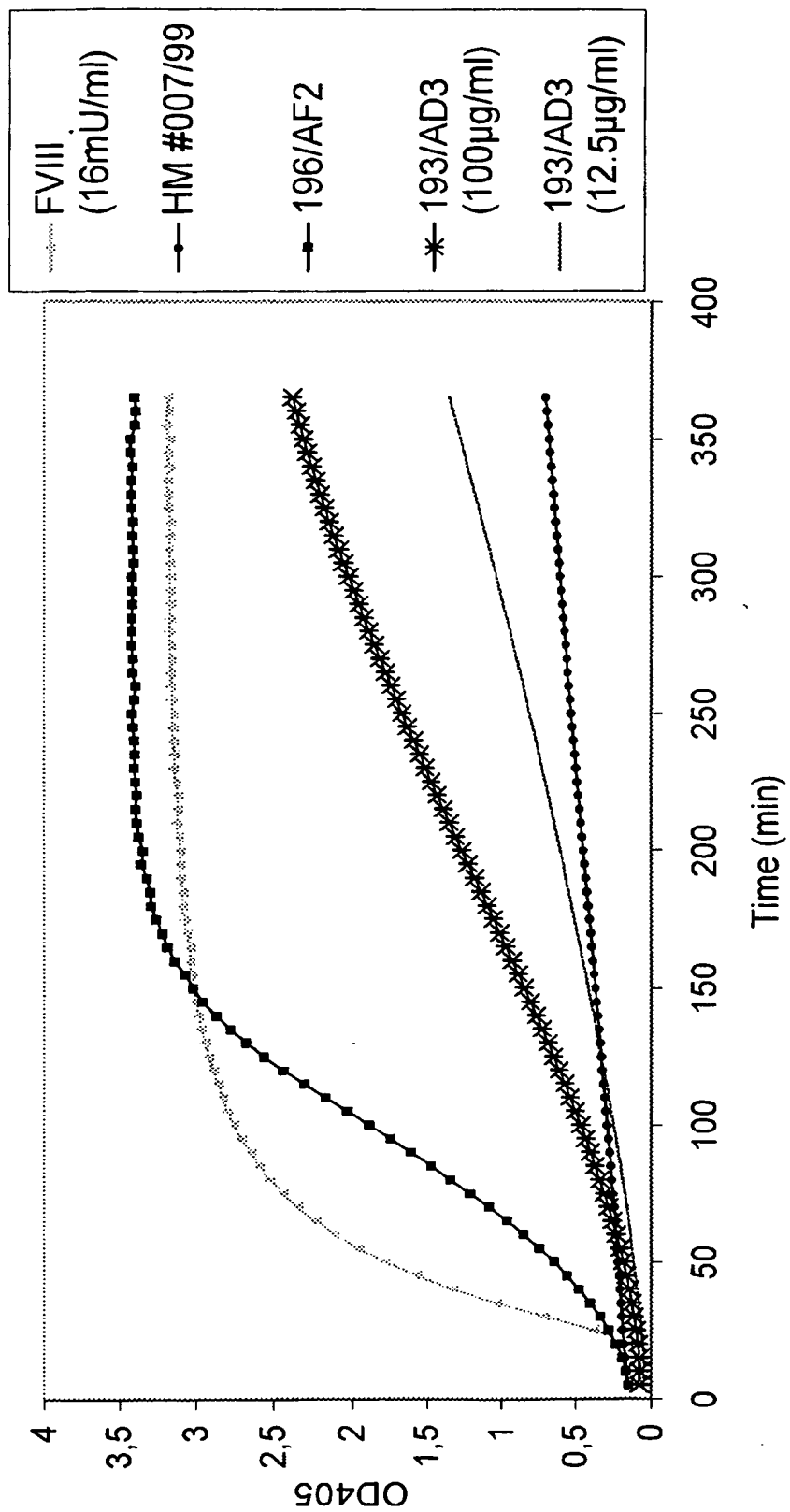


Fig. 6A

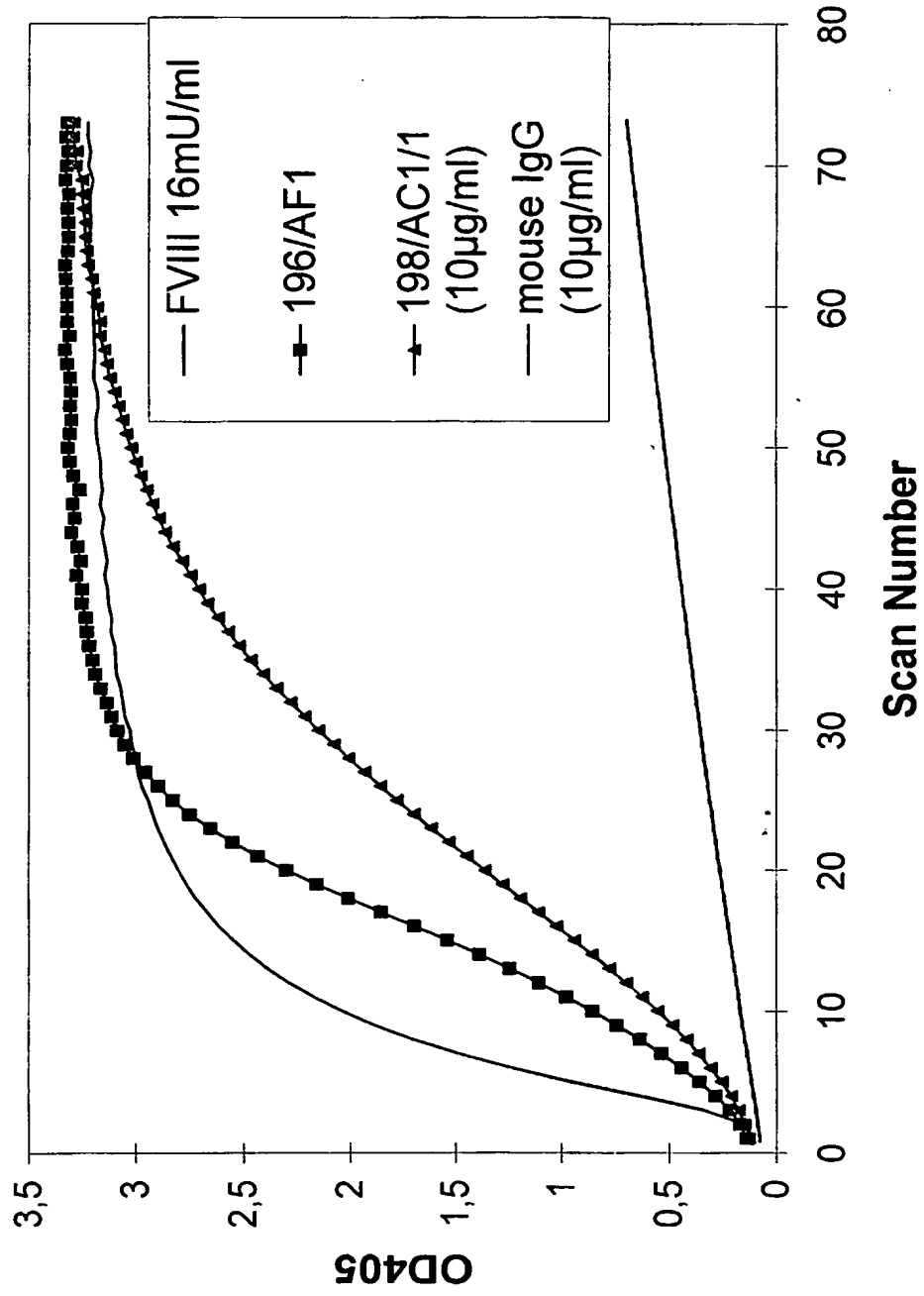


Fig. 6B

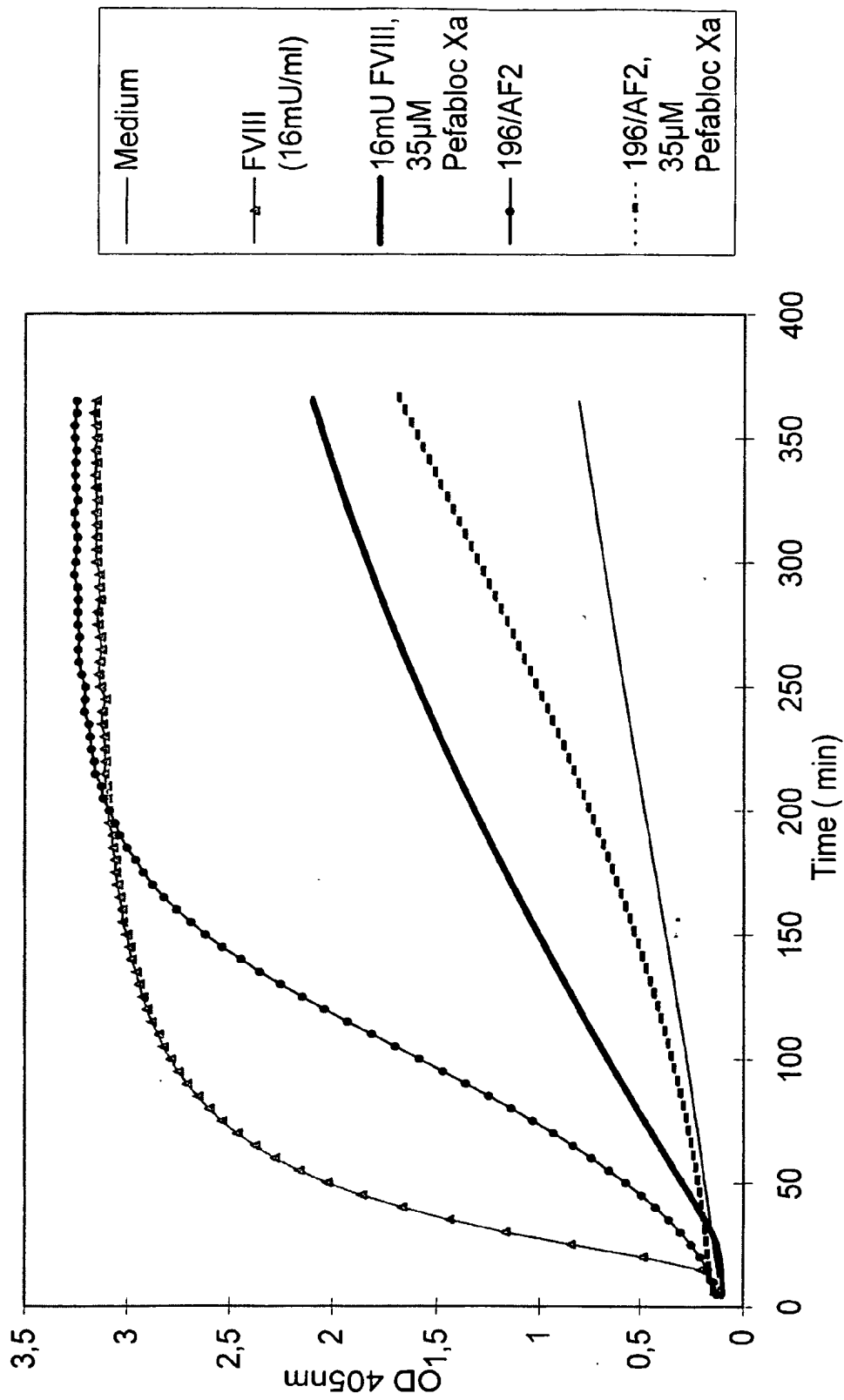


Fig. 7A

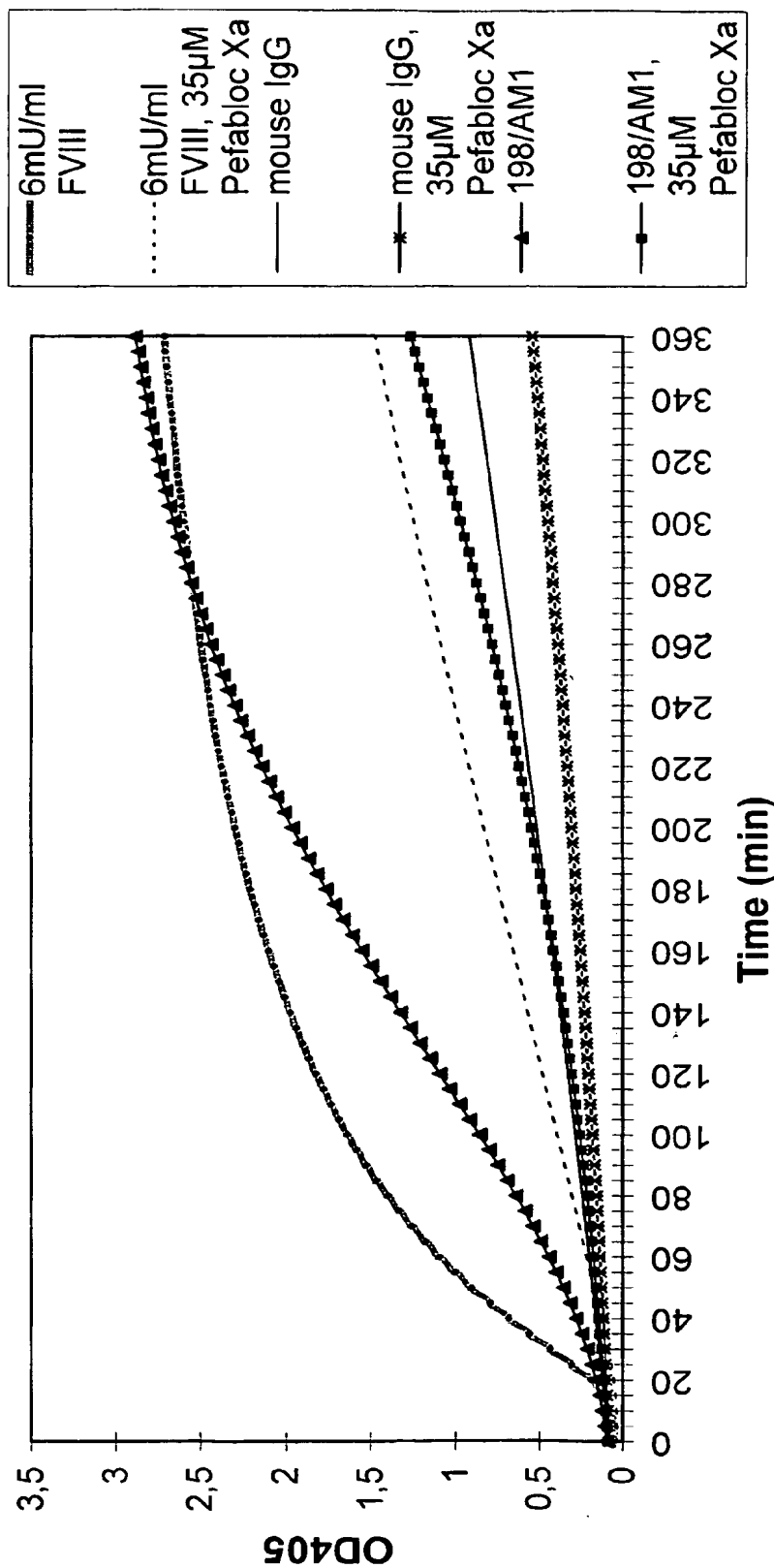


Fig. 7B

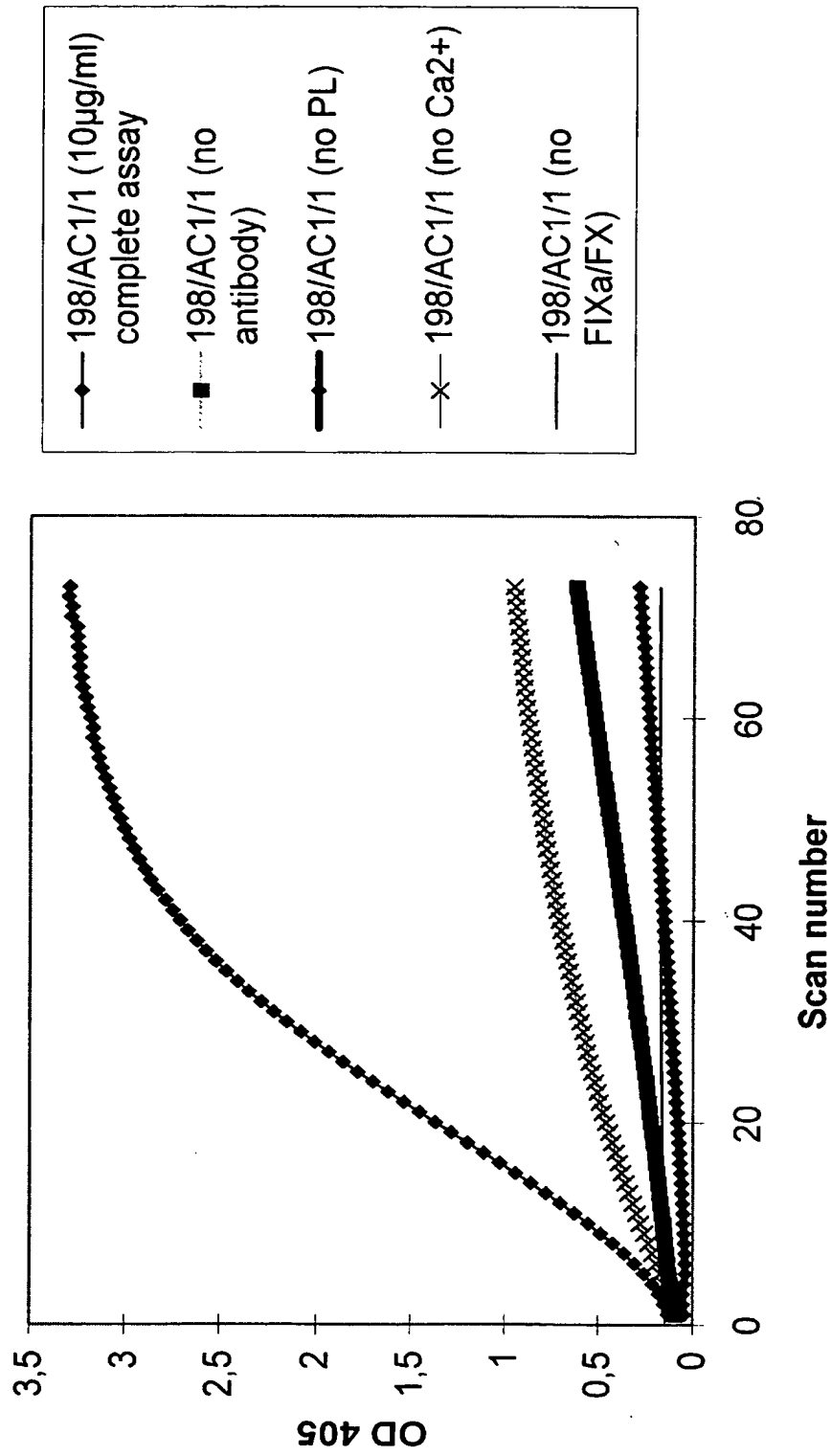


Fig. 8A

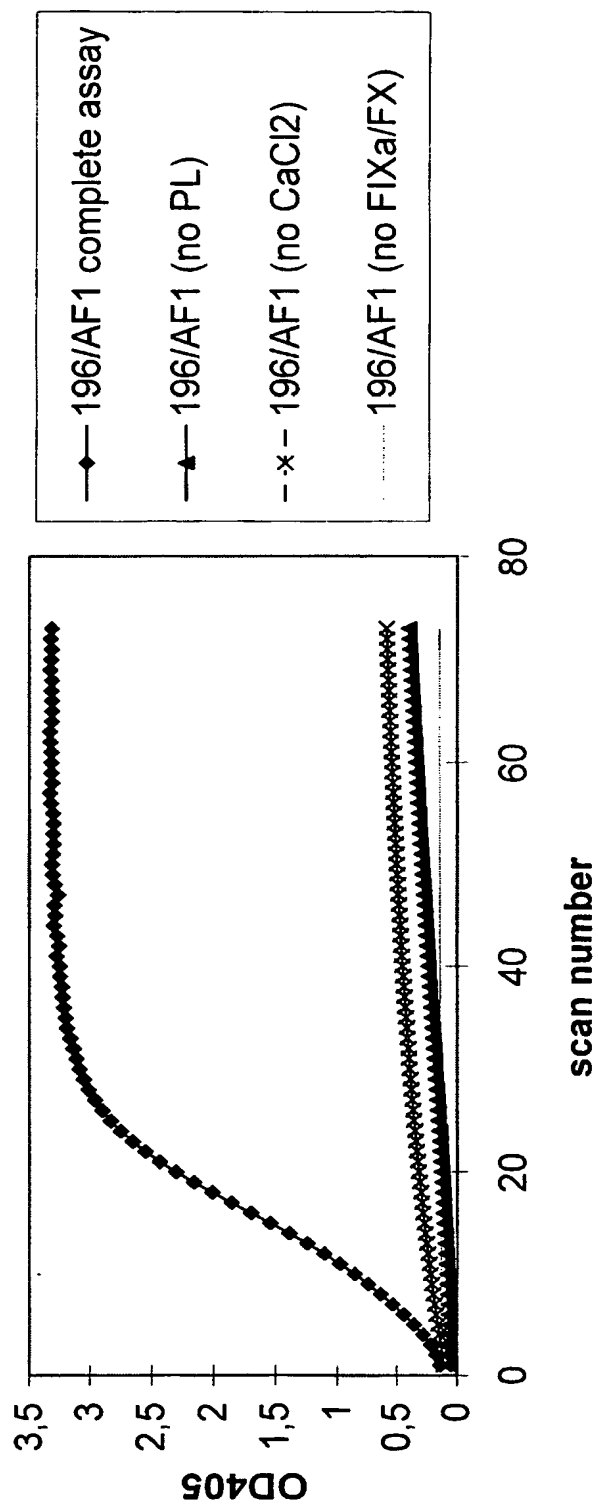


Fig. 8B

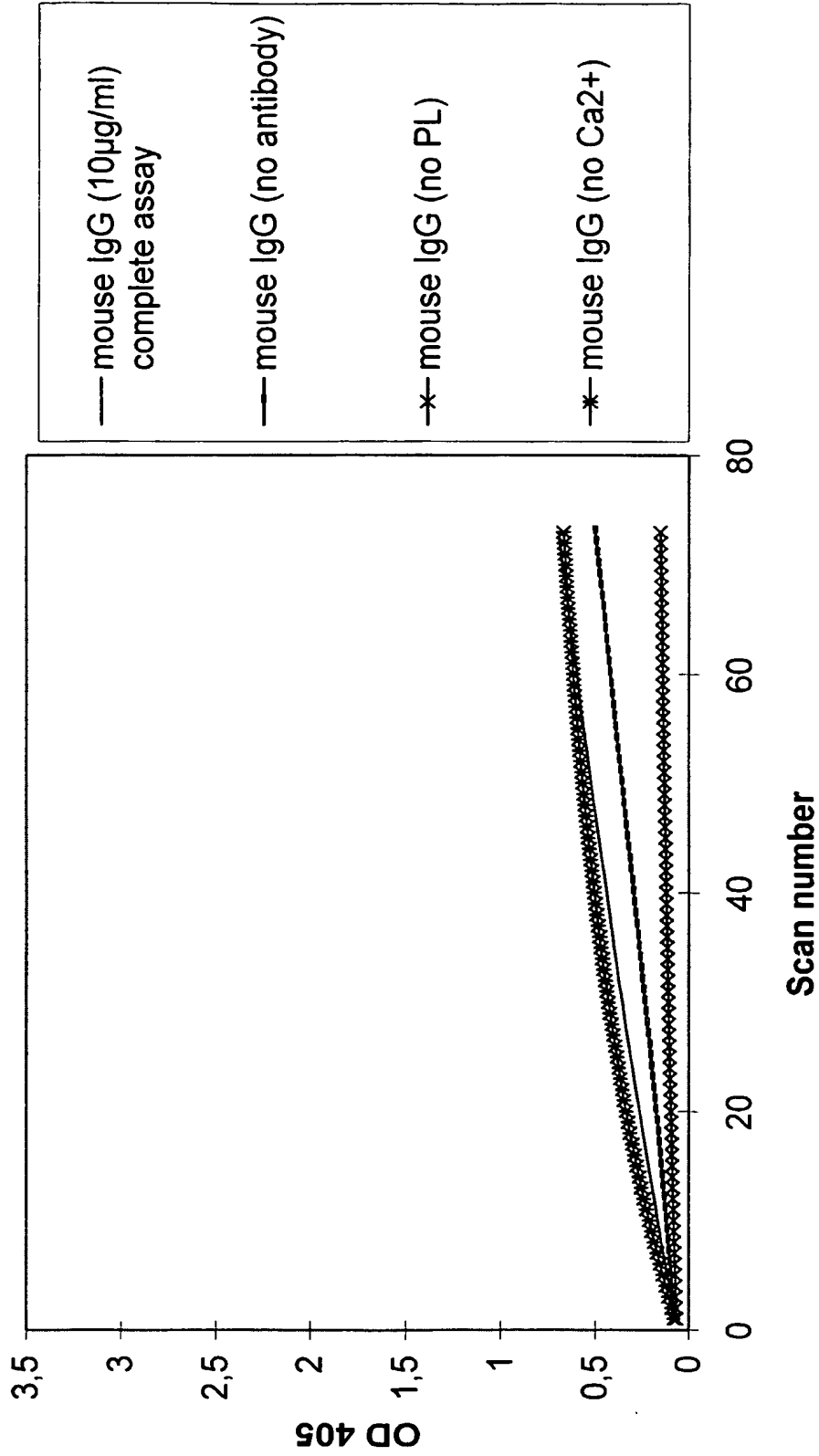


Fig. 8C

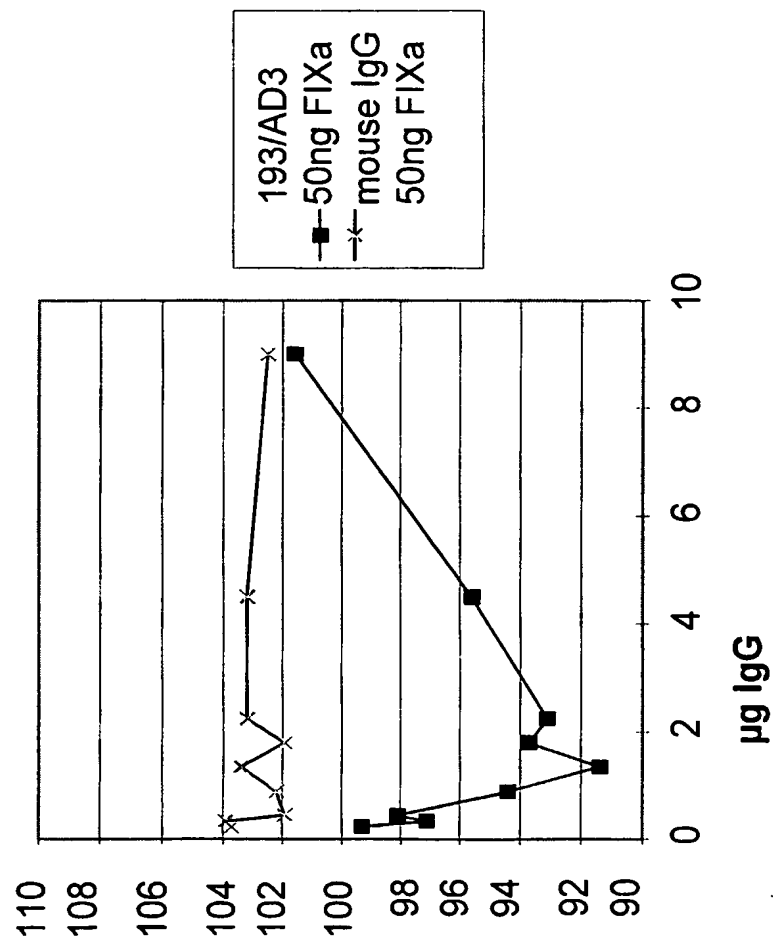


Fig.9

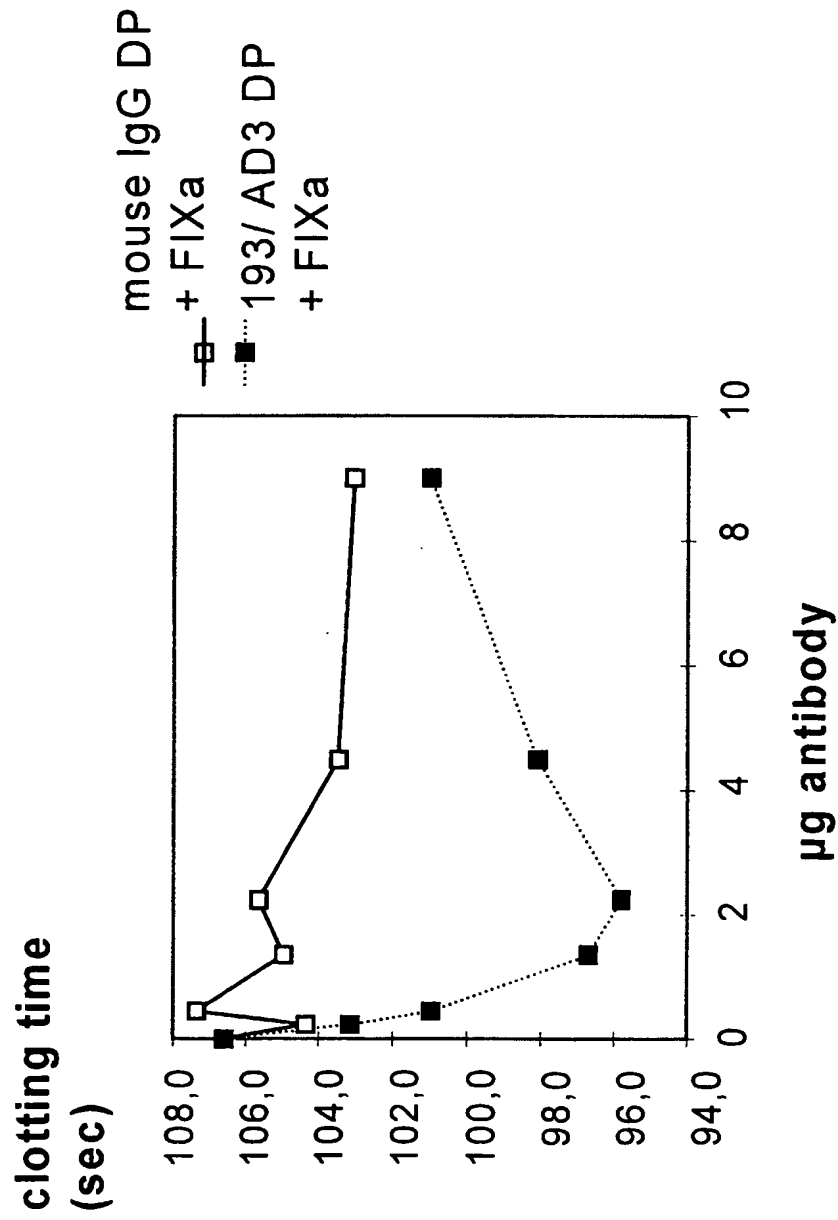


Fig. 10A

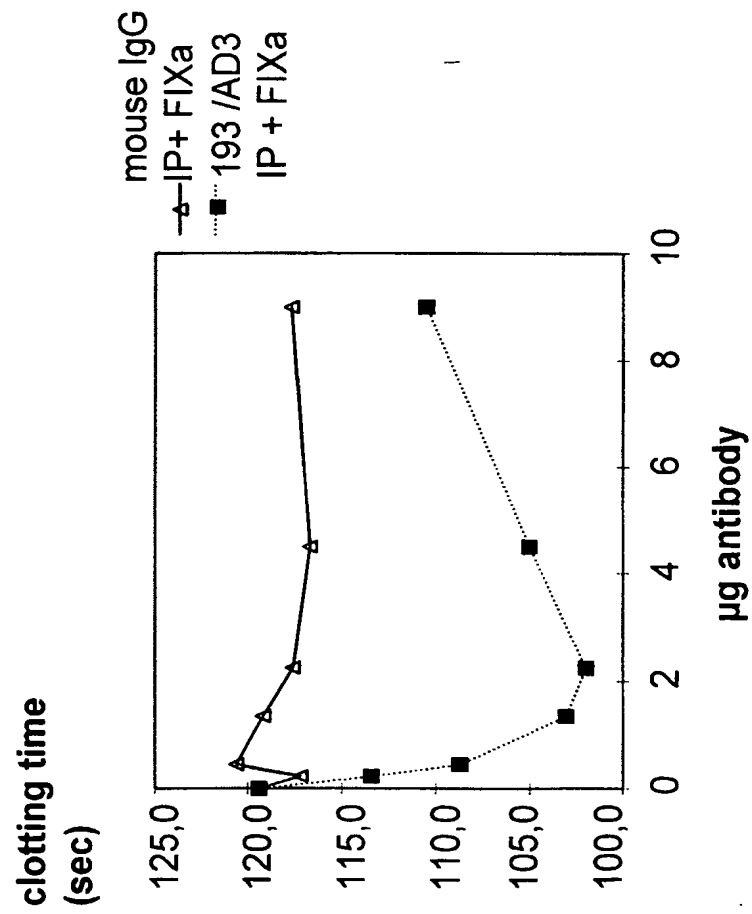


Fig. 10B

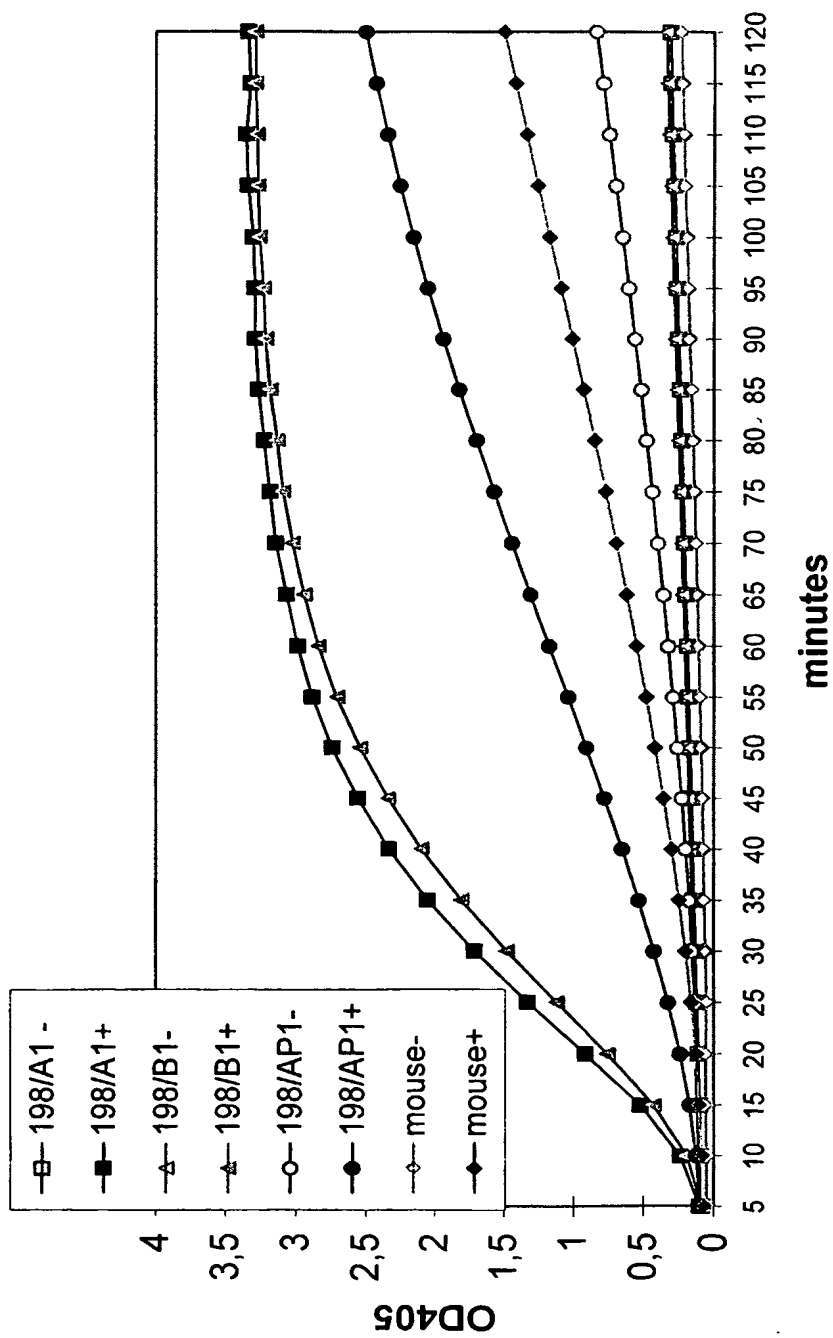


Fig.11

Mouse *V_H* back primers (containing *SfiI*-site):

VH1BACK-SfiI	5' C ATG CCA TGA CTC GCG GCC CAG CCG GCC ATG GCC SAG GTS MAR CTG CAG SAG TCW GG 3' (SEQ.ID.NO. 50)
VH1BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTG CAG CTT CAG GAG TCA GG 3' (SEQ.ID.NO. 51)
VH2BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAT GTG CAG CTT CAG GAG TCR GG 3' (SEQ.ID.NO. 52)
VH3BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG GTG CAG CTG AAG SAG TCA GG 3' (SEQ.ID.NO. 53)
VH4/6BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTY CAG CTG CAR CAR TCT GG 3' (SEQ.ID.NO. 54)
VH5/9BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG GTY CAR CTG CAG CAG YCT GG 3' (SEQ.ID.NO. 55)
VH7BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAR GTG AAG CTG GTG GAR TCT GG 3' (SEQ.ID.NO. 56)
VH8BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTT CAG CTT CAG CAG TCT GG 3' (SEQ.ID.NO. 57)
VH10BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAA GTG CAG CTG KTG GAG WCT GG 3' (SEQ.ID.NO. 58)
VH11BACKSfi	5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG ATC CAG TTG CTG CAG TCT GG 3' (SEQ.ID.NO. 59)

Fig. 12-1

Mouse *J_H* forward primers (containing $\frac{1}{2}$ linker-sequence and *AscI*-site):

VH1FOR2LiAsc	5' ACC GCC AGA GGC GCG CCC ACC TGA ACC GCC TCC ACC TGA GGA GAC GGT GAC CGT GGT CCC TTG GCC CC 3' (SEQ.ID.NO. 60)
JH1FORLiAsc	5' ACC GCC AGA GGC GCG CCC ACC TGA ACC GCC TCC ACC TGA GGA GAC GGT GAC CGT GGT CCC 3' (SEQ.ID.NO. 61)
JH2FORLiAsc	5' ACC GCC AGA GGC GCG CCC ACC TGA ACC GCC TCC ACC TGA GGA GAC TGT GAG AGT GGT GCC 3' (SEQ.ID.NO. 62)
JH3FORLiAsc	5' ACC GCC AGA GGC GCG CCC ACC TGA ACC GCC TCC ACC TGC AGA GAC AGT GAC CAG AGT CCC 3' (SEQ.ID.NO. 63)
JH4FORLiAsc	5' ACC GCC AGA GGC GCG CCC ACC TGA ACC GCC TCC ACC TGA GGA GAC GGT GAC TGA GGT TCC 3' (SEQ.ID.NO. 64)

IUPAC-Code: M=A/C, W=A/T, R=A/G, Y=C/T, S=C/G, K=G/T, H=A/C/T, D=A/G/T, V=A/C/G, B=T/C/G.

Fig. 12-2

Primers for cloning mouse V_k genes

Mouse V_k back primers (containing *AscI*-site and $\frac{1}{2}$ linker-sequence):

VK2BACK-LiAscI	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG GAC ATT GAG CTC ACC CAG TCT CCA 3' (SEQ.ID.NO. 65)
VK1BACKLi Asc	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG GAC ATT GTG ATG WCA CAG TCT CC 3' (SEQ.ID.NO. 66)
VK2BACKLi Asc	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG GAT GTT KTG ATG ACC CAA ACT CC 3' (SEQ.ID.NO. 67)
VK3BACKLi Asc	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG GAT ATT GTG ATR ACB CAG GCW GC 3' (SEQ.ID.NO. 68)
VK4BACKLi Asc	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG GAC ATT GTG CTG ACM CAR TCT CC 3' (SEQ.ID.NO. 69)
VK5BACKLi Asc	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG SAA AWT GTK CTC ACC CAG TCT CC 3' (SEQ.ID.NO. 70)
VK6BACKLi Asc	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG GAY ATY VWG ATG ACM CAG WCT CC 3' (SEQ.ID.NO. 71)
VK7BACKLi Asc	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG CAA ATT GTT CTC ACC CAG TCT CC 3' (SEQ.ID.NO. 72)
VK8BACKLi Asc	5' GGT TCA GAT GGG CGC GCC TCT GGC GGT GGC GGA TCG TCA TTA TTG CAG GTG CTT GTG GG 3' (SEQ.ID.NO. 73)

Fig. 13-1

Mouse J_K forward primers (containing NotI-site):

JK1NOT10	5'	GAG	TCA	TTC	TGC	GGC	CGC	CCG	TTT	GAT	TTC	CAG	CTT	GGT	CCC	3'
		(SEQ.ID.NO. 74)														
JK2NOT10	5'	GAG	TCA	TTC	TGC	GGC	CGC	CCG	TTT	TAT	TTC	CAG	CTT	GGT	CCC	3'
		(SEQ.ID.NO. 75)														
JK3NOT10	5'	GAG	TCA	TTC	TGC	GGC	CGC	CCG	TTT	TAT	TTC	CAG	TCT	GGT	CCC	3'
		(SEQ.ID.NO.76)														
JK4NOT10	5'	GAG	TCA	TTC	TGC	GGC	CGC	CCG	TTT	TAT	TTC	CAA	CTT	TGT	CCC	3'
		(SEQ.ID.NO. 77)														
JK5NOT10	5'	GAG	TCA	TTC	TGC	GGC	CGC	CCG	TTT	CAG	CTC	CAG	CTT	GGT	CCC	3'
		(SEQ.ID.NO. 78)														

IUPAC-Code: K=G/T, M=A/C, W=A/T, R=A/G, Y=C/T, S=C/G, H=A/C/T, D=A/G/T, V=A/C/G, B=T/C/G.

Fig. 13-2

VH

```

+1  E V K L V E S G P E L K K P G
1   GAG GTG AAG CTG GTG GAG TCT GGA CCT GAG CTG AAG AAG CCT GGA

+1  E T V K I S C K A S G Y I F T
46  GAG ACA GTC AAG ATC TCC TGC AAG GCT TCT GGG TAT ATC TTC ACA

+1  N Y G M N W V K Q A P G K G L
91  AAC TAT GGA ATG AAC TGG GTG AAG CAG GCT CCA GGA AAG GGT TTA

+1  K W M G W I N T Y T G E P T Y
136 AAG TGG ATG GGC TGG ATA AAC ACC TAC ACT GGA GAG CCA ACA TAT

+1  A D D F K G R F A F S L E T S
181 GCT GAT GAC TTC AAG GGA CGG TTT GCC TTC TCT TTG GAA ACC TCT

+1  A S T A Y L Q I N N L K N E D
226 GCC AGC ACT GCC TAT TTG CAG ATC AAC AAC CTC AAA AAT GAG GAC

+1  T A T Y F C A L Y G N S P K G
271 ACG GCT ACA TAT TTC TGT GCA TTA TAT GGT AAC TCC CCT AAG GGG

+1  F A Y W G Q G T L V T V S A G
316 TTT GCT TAC TGG GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA GGT

+1  G G G S G G R A S G G G G S D
361 GGA GGC GGT TCA GGT GGG CGC GCC TCT GGC GGT GGC GGA TCG GAT

+1  I Q M T Q S P K F L L V S A G
406 ATT CAG ATG ACA CAG TCT CCC AAA TTC CTG CTT GTA TCA GCA GGA

```

Fig. 14-1

```

+1   D   R   V   T   I   T   C   K   A   S   Q   S   V   S   N
451  GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG AGT AAT

+1   D   V   A   W   Y   Q   Q   K   P   G   Q   S   P   K   L
496  GAT GTA GCT TGG TAC CAA CAG AAG CCG GGG CAG TCT CCT AAA CTA

+1   L   M   Y   Y   A   S   N   R   Y   T   G   V   P   D   R
541  CTG ATG TAC TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC

+1   F   T   G   S   G   Y   G   T   D   F   T   F   T   I   S
586  TTC ACT GGC AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC

+1   T   V   Q   A   E   D   L   A   V   Y   F   C   Q   Q   D
631  ACT GTG CAG GCT GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT

+1   Y   G   S   P   P   T   F   G   G   T   K   L   E   I
676  TAT GGC TCT CCT CCC ACG TTC GGA GGG GGC ACC AAG CTG GAA ATT

+1   K   R
721  AAA CGG

```

Fig. 14 -2

VH
 +1 E V Q L V E S G G G L V K P G
 1 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC CTA GTG AAG CCT GGA

 +1 G S L K L S C A A S G F T F S
 46 GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT GGA TTC ACT TTC AGT

 +1 T Y T M S W V R Q T P E K R L
 91 ACC TAT ACC ATG TCT TGG GTT CGC CAG ACT CCG GAG AAG AGG CTG

 +1 E W V A T I S S G G S Y T Y Y
 136 GAG TGG GTC GCA ACC ATT AGT AGT GGT GGT TAC ACC TAC TAT

 +1 P D S V R G R F T I S R D N A
 181 CCA GAC AGT GTG AGG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC

 +1 K N T L Y L Q M S S L K S E D
 226 AAG AAC ACC CTG TAC CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC

 +1 T A M Y Y C T R D G G H G Y G
 271 ACA GCC ATG TAT TAC TGT ACA AGA GAT GGG GGA CAC GGG TAC GGT

 +1 S S F D Y W G Q G T T L T V S
 316 AGT AGC TTT GAC TAC TGG GGC CAA GGC ACC ACT CTC ACA GTC TCC

 linker ..
 +1 S G G G S G G R A S G G G
 361 TCA GGT GGA GGC GGT TCA GGT GGG CGC GCC TCT GGC GGT GGC GGA

 VL
 +1 S Q I V L T Q S P L S L P V S
 406 TCG CAA ATT GTG CTC ACC CAG TCT CCA CTC TCC CTG CCT GTC AGT

Fig. 15-1

```

+1   L   G   D   Q   A   S   I   S   C   R   S   S   Q   S   I
451  CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT

+1   V   H   S   N   G   N   T   Y   L   E   W   Y   L   Q   K
496  GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTG CAG AAA

+1   P   G   Q   S   P   K   L   L   I   Y   K   V   S   N   R
541  CCA GGC CAG TCT CCA AAG CTC CTG ATC TAC AAA GTT TCC AAC CGA

+1   F   S   G   V   P   D   K   F   S   G   S   G   S   G   T
586  TTT TCT GGG GTC CCA GAC AAA TTC AGT GGC AGT GGA TCA GGG ACA

+1   D   F   T   L   K   I   S   R   V   E   A   E   D   L   G
631  GAT TTC ACA CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA

+1   V   Y   Y   C   F   Q   G   S   H   V   P   W   T   F   G
676  GTT TAT TAC TGC TTT CAA GGT TCA CAT GTT CCG TGG ACG TTC GGT

1    G   G   T   K   L   E   I   K   R
721  GGA GGC ACC AAG CTG GAA ATC AAA CGG

```

Fig. 15-2

```

+1 E V Q L Q E S G G L V K P G
1 GAG GTG CAG CTT CAG GAG TCA GGG GGA GGC TTA GTG AAG CCT GGA

+1 G S L K L S C A A S G F T F S
46 GGG TCC CTG AAA CTC TCC TGT GCA GCC TCT GGA TTC ACT TTC AGT

+1 S Y T M S S W V R Q T P E K R L
91 AGC TAT ACC ATG TCT TGG GTT CGC CAG ACT CCG GAG AAG AGG CTG

+1 E W V A T I S S G G S S T Y Y
136 GAG TGG GTC GCA ACC ATT AGT AGT GGT GGT AGT TCC ACC TAC TAT

+1 P D S V K G R F T I S R D N A
181 CCA GAC AGT GTG AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC

+1 K N T L Y L Q M S S L R S E D
226 AAG AAC ACC CTG TAC CTG CAA ATG AGC AGT CTG AGG TCT GAG GAC

+1 T A M Y Y C T R E G G G F T V
271 ACA GCC ATG TAT TAC TGT ACA AGA GAG GGG GGT TTC ACC GTC

+1 N W Y F D V W G A G T L V T V
316 AAC TGG TAC TTC GAT GTC TGG GGC GCA GGG ACT CTG GTC ACT GTC

linker
+1 S A G G G G S G G R A S G G G
361 TCT GCA GGT GGA GGC GGT TCA GGT GGG CGC GCC TCT GGC GGT GGC

VL
+1 G S E N V L T Q S P A S L A V
406 GGA TCG GAA AAT GTG CTC ACC CAG TCT CCA GCT TCT TTG GCT GTG

```

Fig. 16-1

```

+1 S L G Q R A T I S C R A S E S
451 TCT CTA GGG CAG AGG GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT

+1 V D S Y G Y N F M H W Y Q Q I
496 GTT GAT AGT TAT GGC TAT AAT TTT ATG CAC TGG TAT CAG CAG ATA

+1 P G Q P P K L L I Y R A S N L
541 CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT CGT GCA TCC AAC CTA

+1 E S G I P A R F S G S G S R T
586 GAG TCT GGG ATC CCT GCC AGG TTC AGT GGC AGT GGC TCT AGG ACA

+1 D F T L T I N P V E A D D V A
631 GAC TTC ACC CTC ACC ATT AAT CCT GTG GAG GCT GAT GAT GTT GCA

+1 T Y Y C Q Q S N E D P L T F G
676 ACC TAT TAC TGT CAG CAA AGT AAT GAG GAT CCG CTC ACG TTC GGT

+1 T G T R L E I K R
721 ACT GGG ACC AGA CTG GAA ATA AAA CGG

```

Fig.16 -2

VH

+1 E V Q L Q E S G G L V K P G G S L K L
 1 GAG GTG CAG CTT CAG GAG TCA GGG GGA CCT GGA GGG TCC CTG AAA CTC
 CTC CAC GTC GAA GTC CTC AGT CCC CCT CCG AAT CAC TTC GGA CCT CCC AGG GAC TTT GAG

+1 S C A A S G F I F S S Y T M S W V R Q T
 61 TCC TGT GCA GCC TCT GGA TTC ATT TTT AGT AGT TAT ACC ATG TCT TGG GTT CGC CAG ACT
 AGG ACA CGT CGG AGA CCT AAG TAA AAA TCA TCA ATA TGG TAC AGA ACC CAA GCG GTC TGA

+1 P E K R L E W V A T I S S G G S S T Y Y
 121 CCG GAG AAG AGG CTG GAG TGG GTC GCA ACC ATT AGT AGT GGT GGT TCC ACC TAC TAT
 GGC CTC TTC TCC GAC CTC ACC CAG CGT TGG TAA TCA TCA CCA TCA AGG TGG ATG ATA

+1 P D S V K G R F T I S R D N A K N T L Y
 181 CCA GAC AGT GTG AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTG TAC
 GGT CTG TCA CAC TTC CCG GCT AAG TGG TAG AGG TCT CTG TTA CGG TTC TTT TGG GAC ATG

+1 L Q M S S L K S E D T A M Y H C T R E G
 241 CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC ACA GCC ATG TAT CAC TGT ACA AGA GAG GGG
 GAC GTT TAC TCG TCA GAC TTC AGA CTC CTG TGT CGG TAC ATA GTG ACA TGT TCT CTC CCC

+1 G G Y Y V N W Y F D V W G A G T T L T V
 301 GGT GGT TAT TAC GTC AAC TGG TAC TTC GAT GTC TGG GGC GCA GGC ACC ACT CTC ACA GTC
 CCA CCA ATA ATG CAG TTG ACC ATG AAG CTA CAG ACC CCG CGT CCG TGG TGA GAG TGT CAG

linker

+1 S S G G G G S S G G R A S G G G S D I E
 361 TCC TCA GGT GGA GGC GGT TCA GGT GGC CGC GCC TCT GGC GGT GGC GGA TCG GAC ATT GAG
 AGG AGT CCA CCT CCG CCA AGT CCA CCC GCG CGG AGA CCG CCA CCG CCT AGC CTG TAA CTC

+1 L T Q S P A S L A V S L G Q R A T I S C
 421 CTC ACN CAG TCT CCA GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG GCC ACC ATA TCC TGC
 GAG TGN GTC AGA GGT CGA AGA AAC CCA CAC AGA GAT CCC GTC TCC CGG TGG TAT AGG ACG

Fig. 17-1

```

+1  R  A  S  E  S  V  D  S  Y  G  K  S  F  M  H  W  Y  Q  Q  K
481  AGA GCC AGT GAA AGT GTT GAT AGT TAT GGC AAG AGT TTT ATG CAC TGG TAC CAG CAG AAA
    TCT CGG TCA CTT TCA CAA CTA TCA ATA CCG TTC TCA AAA TAC GTG ACC ATG GTC GTC TTT

+1  P  G  Q  P  P  K  L  L  I  Y  R  A  S  N  L  E  S  G  I  P
541  CCA GGG CAG CCA CCC AAA CTC CTC ATC TAT CGT GCA TCC AAC CTA GAA TCT GGG ATC CCT
    GGT CCC GTC GGT GGT TTT GAG GAG TAG ATA GCA CGT AGG TTG GAT CTT AGA CCC TAG GGA

+1  A  R  F  S  G  S  G  S  R  T  D  F  T  L  T  I  N  P  V  E
601  GCC AGG TTC AGT GGC AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC ATT AAT CCT GTG GAG
    CGG TCC AAG TCA CCG TCA CCC AGA TCC TGT CTG AAG TGG GAG TGG TAA TTA GGA CAC CTC

+1  A  D  D  V  A  T  Y  Y  C  Q  Q  S  N  E  D  P  L  T  F  G
661  GCT GAT GAT GTT GCN ACC TAT TAC TGT CAG CAA AGT AAT GAG GAT CCC CTC ACG TTC GGT
    CGA CTA CTA CAA CGN TGG ATA ATG ACA GTC GTT TCA TTA CTC CTA GGG GAG TGC AAG CCA

+1  A  G  T  R  L  E  I  K  R
721  GCT GGG ACC AGA CTG GAA ATA AAA CGG
    CGA CCC TGG TCT GAC CTT TAT TTT GCC

```

Fig. 17-2

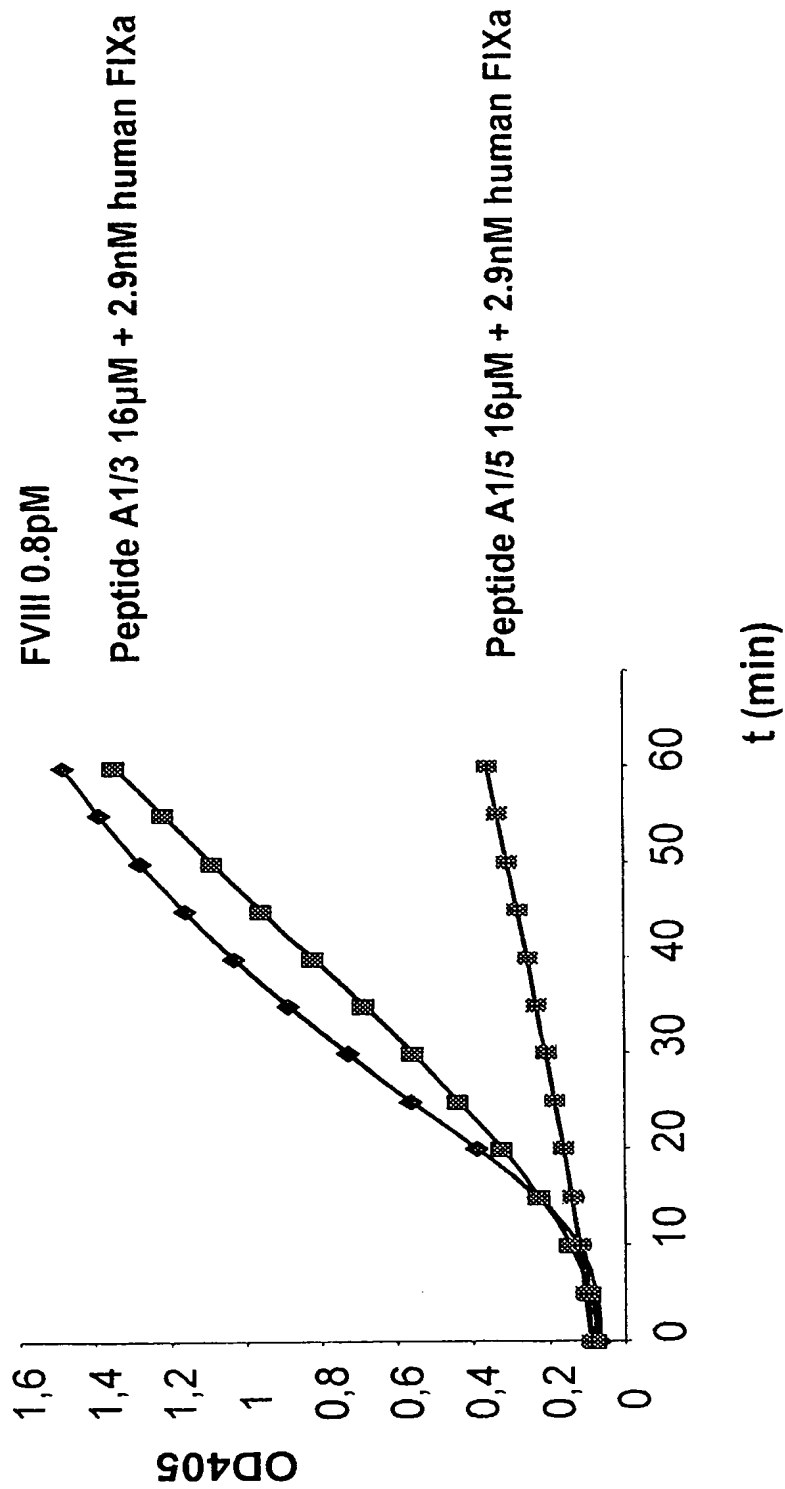


Fig. 18

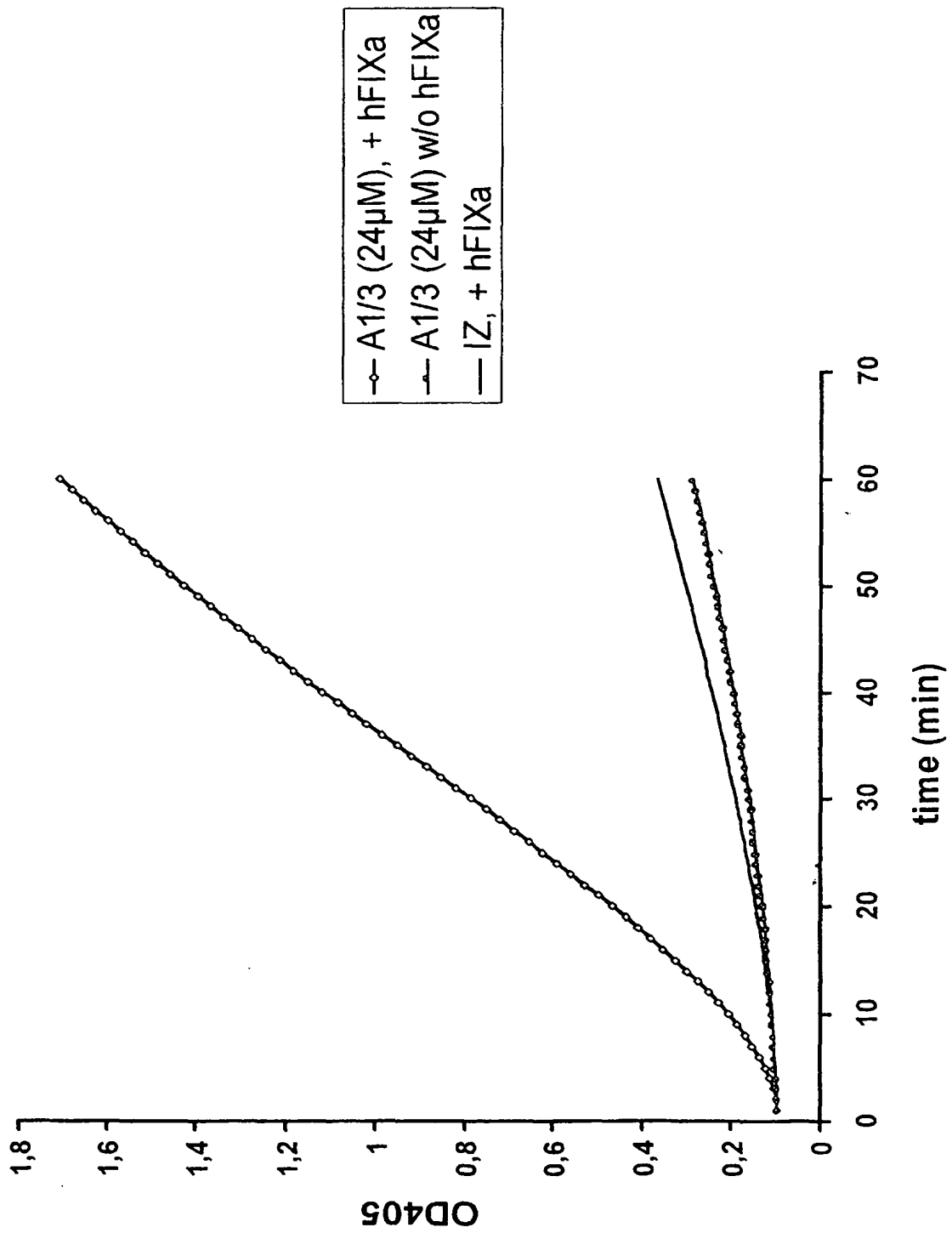


Fig. 19

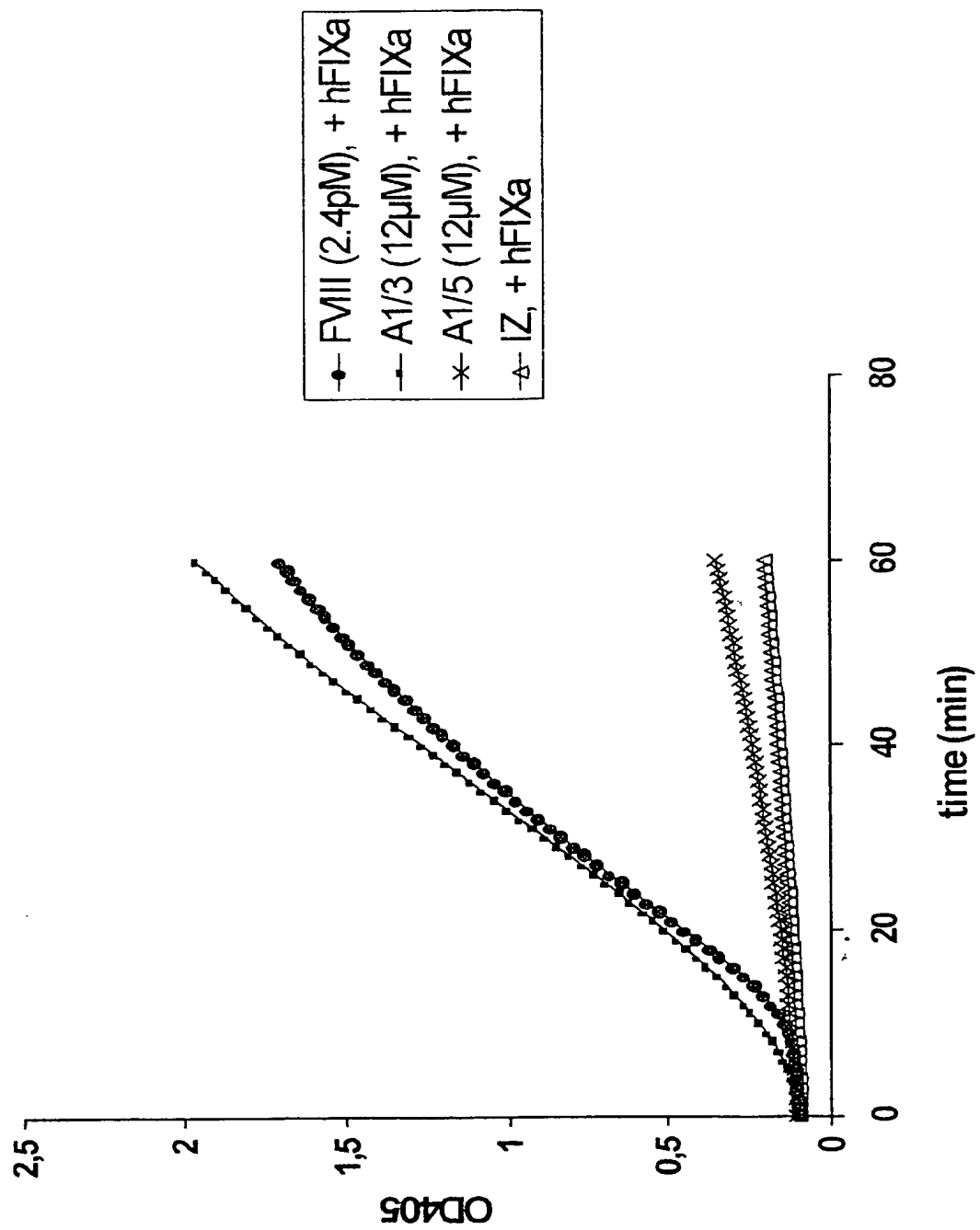


Fig. 20

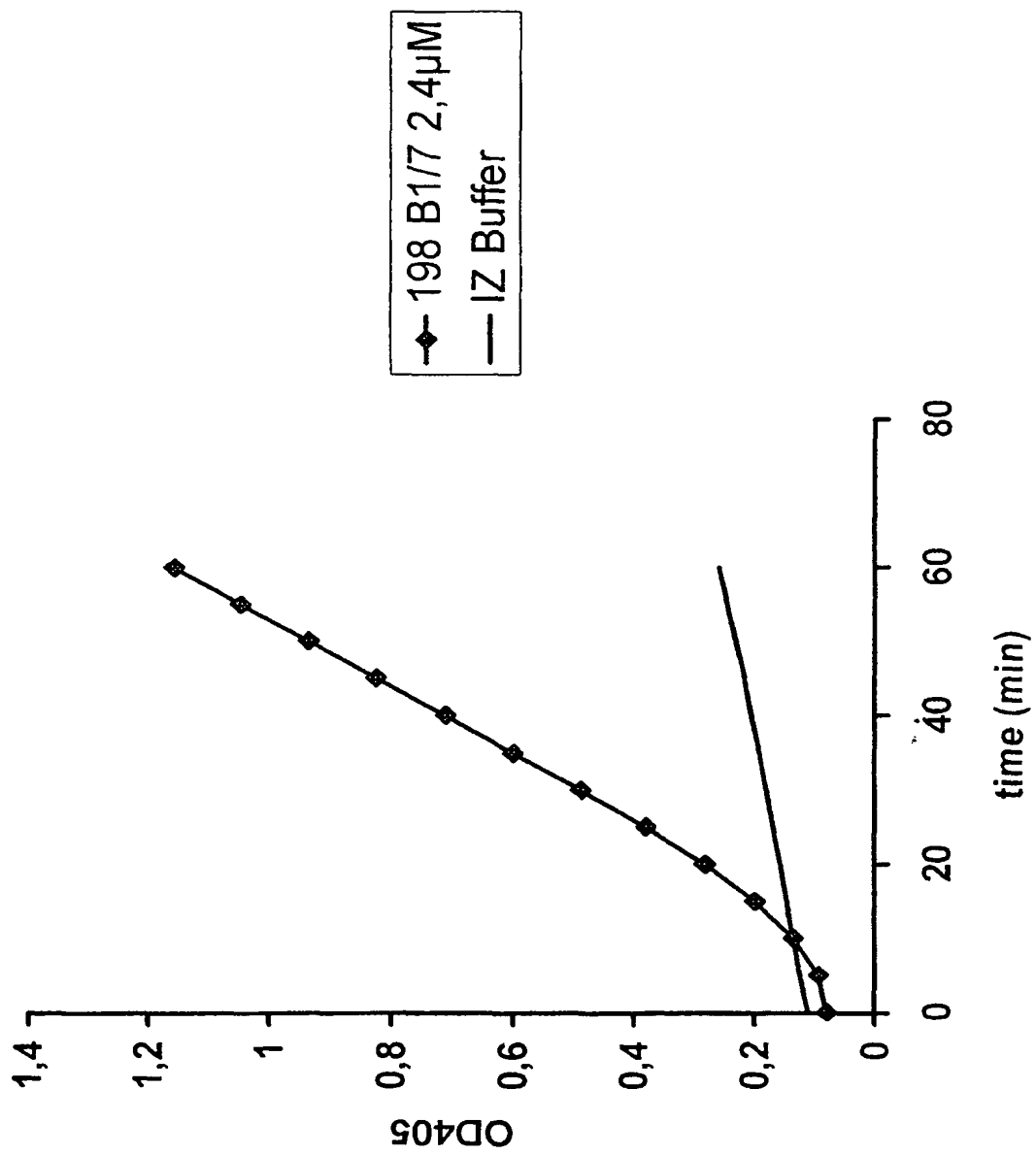


Fig. 21

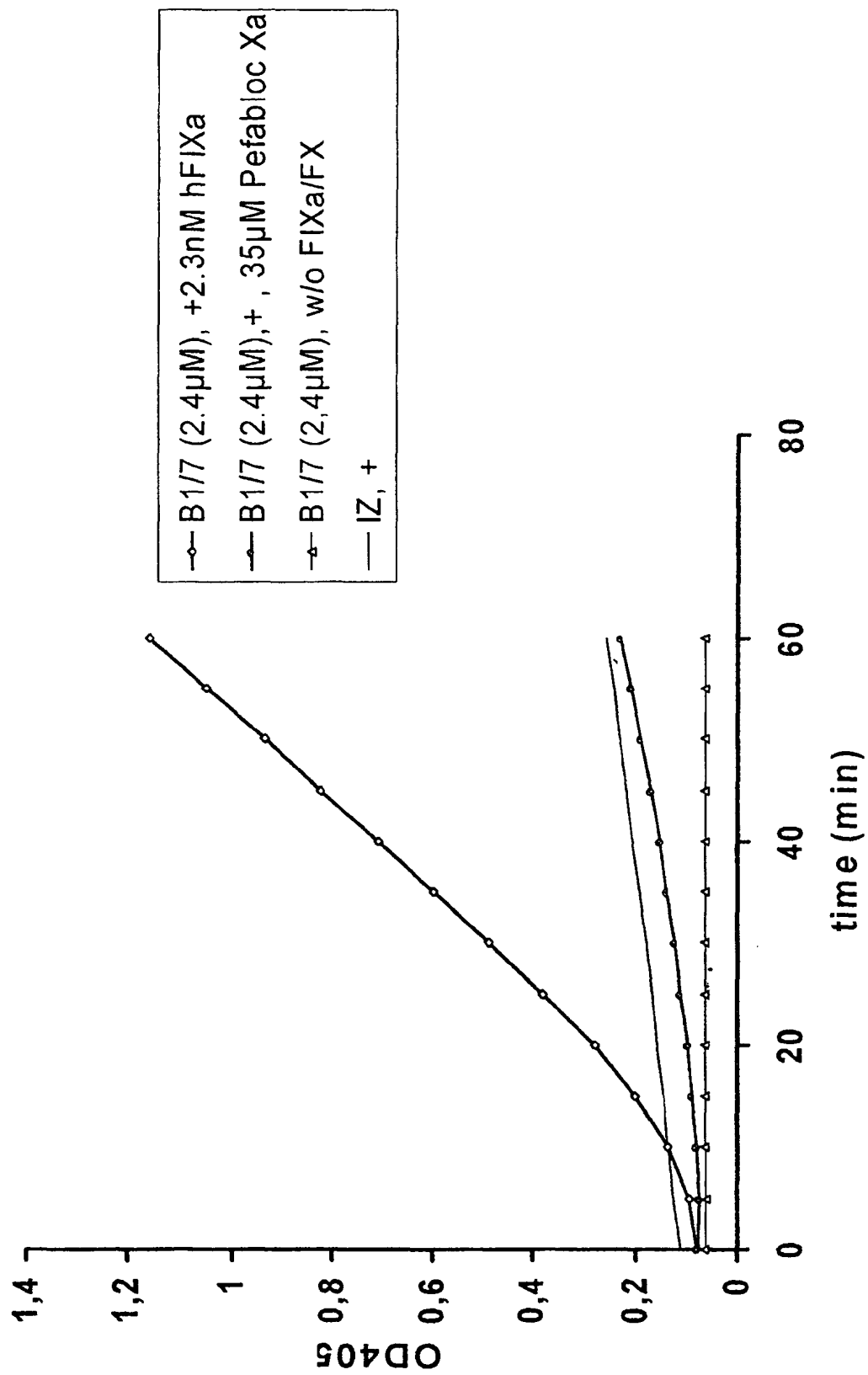


Fig. 22

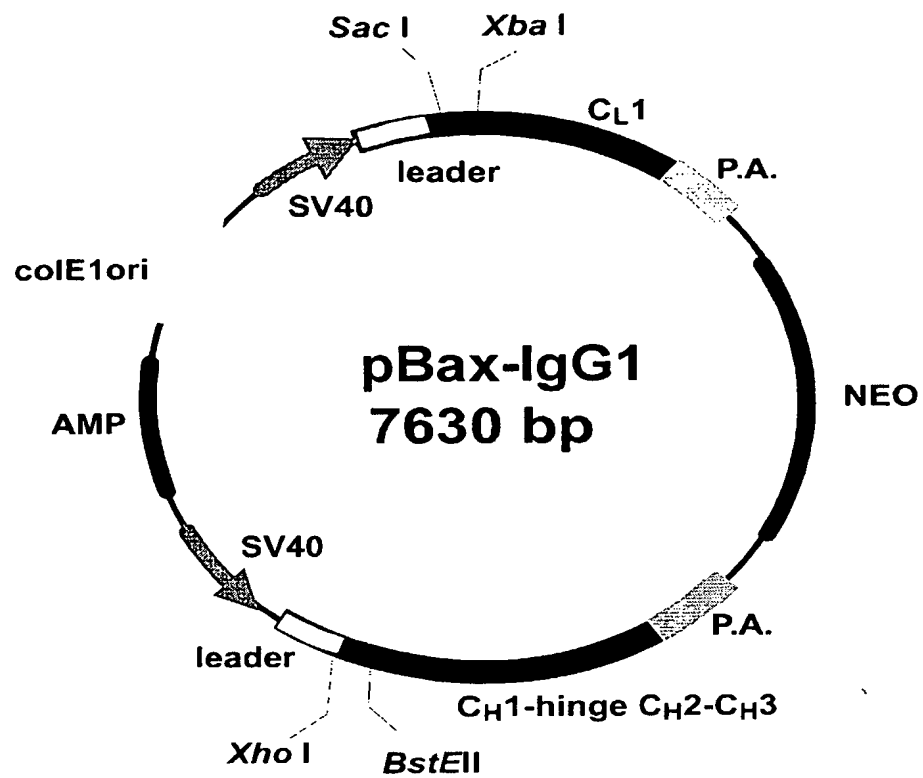


Figure 23

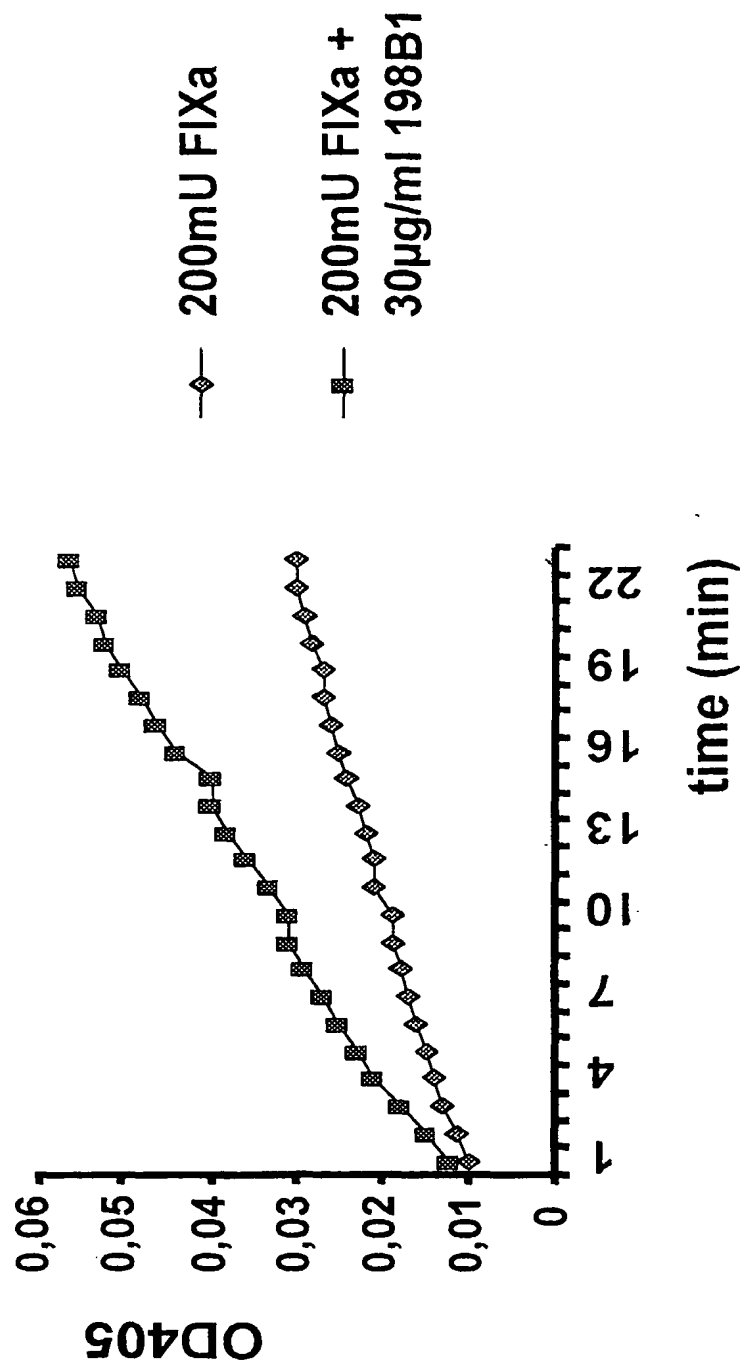


Fig. 24A

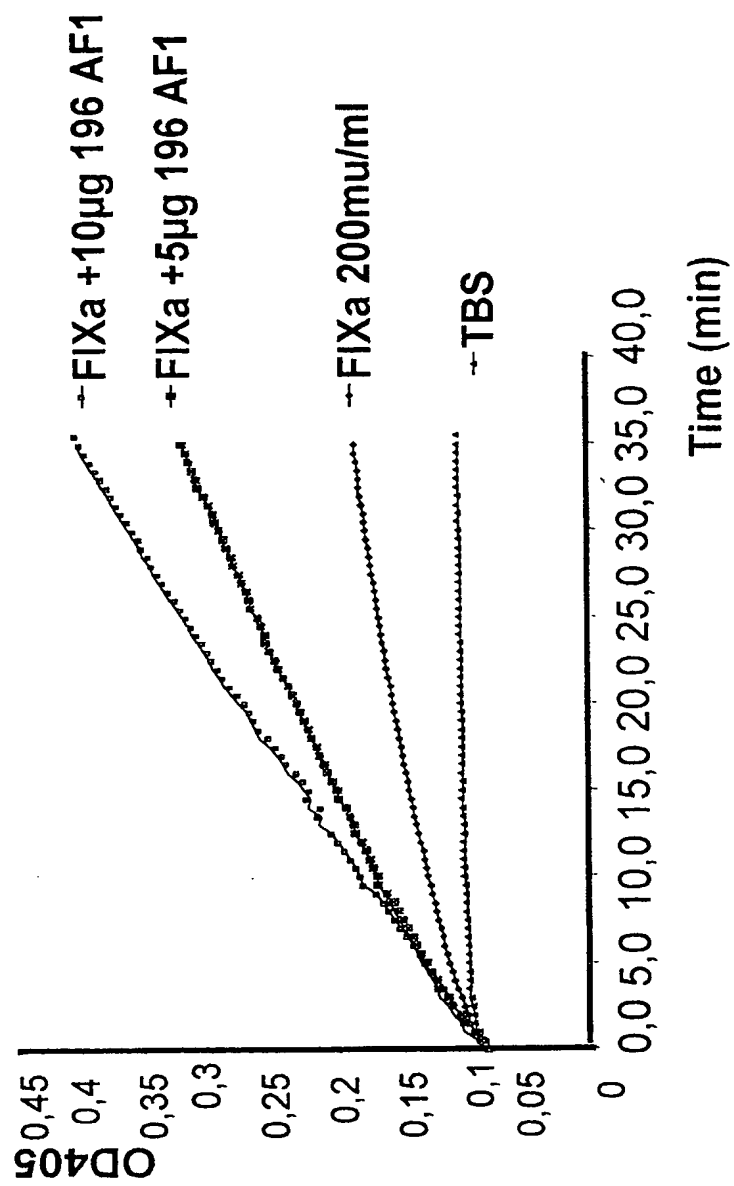


Fig. 24B

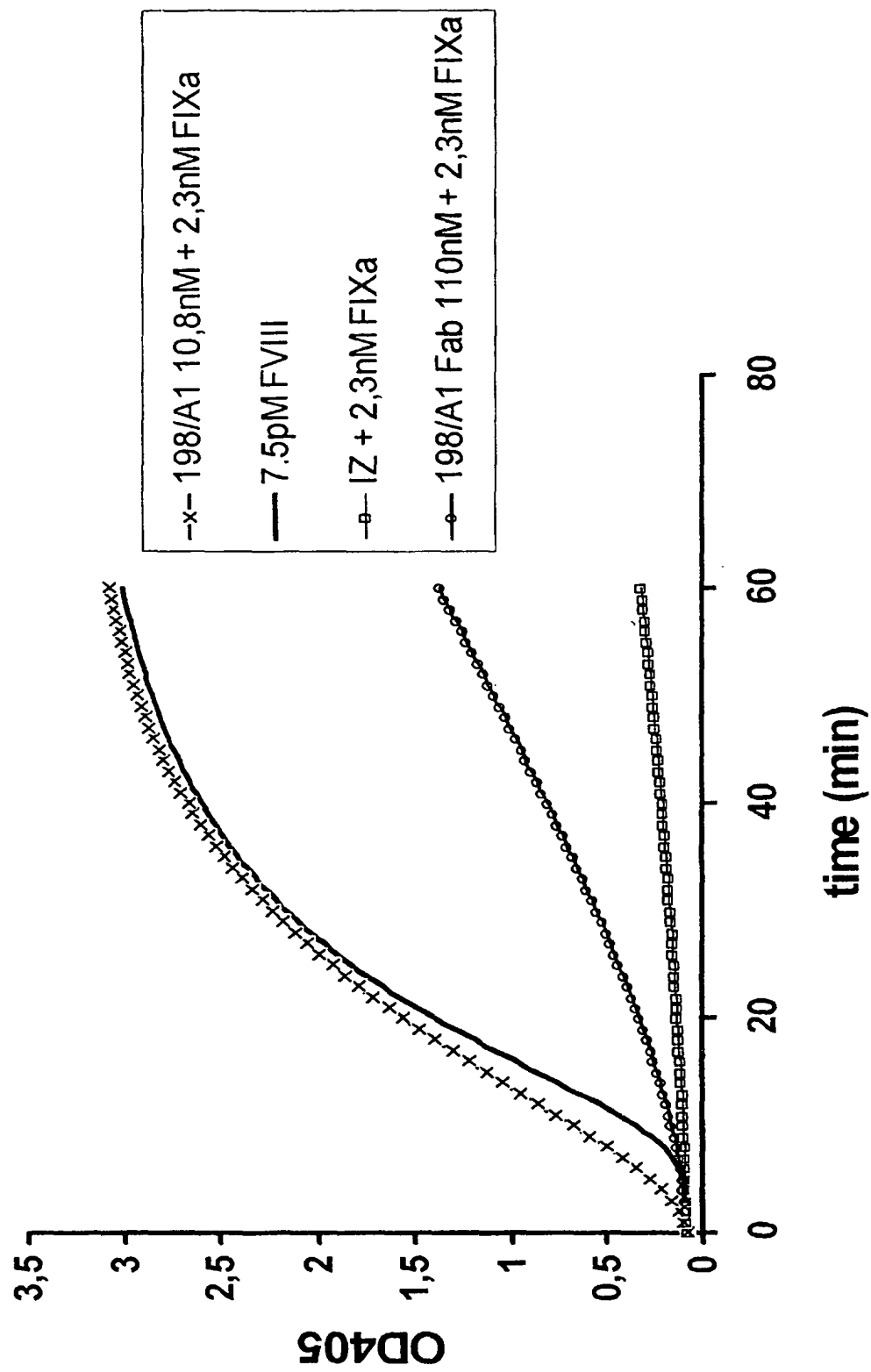


Fig. 25

PelB-leader														
+1	M	K	Y	L	L	P	T	A	A	A	G	L	L	L
1	ATG	AAA	TAC	CTA	TTG	CCT	ACG	GCA	GCC	GCT	GGA	TTG	TTA	TTA
	TAC	TTT	ATG	GAT	AAC	GGA	TGC	CGT	CGG	CGA	CCT	AAC	AAT	AAT
VH														
+1	L	A	A	Q	P	A	M	A	E	V	K	L	V	E
43	CTC	GCG	GCC	CAG	CCG	GCC	ATG	GCG	GAG	GTG	AAG	CTG	GTG	GAG
	GAG	CGC	CGG	GTC	GGC	CGG	TAC	CGC	CTC	CAC	TTC	GAC	CAC	CTC
+1	S	G	G	G	L	V	K	P	G	G	S	L	K	L
85	TCT	GGG	GGA	GGC	TTA	GTG	AAG	CCT	GGA	GGG	TCC	CTG	AAA	CTC
	AGA	CCC	CCT	CCG	AAT	CAC	TTC	GGA	CCT	CCC	AGG	GAC	TTT	GAG
+1	S	C	A	A	S	G	F	T	F	S	S	Y	T	M
127	TCC	TGT	GCA	GCC	TCT	GGA	TTC	ACT	TTC	AGT	AGC	TAT	ACC	ATG
	AGG	ACA	CGT	CGG	AGA	CCT	AAG	TGA	AAG	TCA	TCG	ATA	TGG	TAC
+1	S	W	V	R	Q	T	P	E	K	R	L	E	W	V
169	TCT	TGG	GTT	CGC	CAG	ACT	CCG	GAG	AAG	AGG	CTG	GAG	TGG	GTC
	AGA	ACC	CAA	GCG	GTC	TGA	GGC	CTC	TTC	TCC	GAC	CTC	ACC	CAG
+1	A	T	I	S	S	G	G	S	S	T	Y	Y	P	D
211	GCA	ACC	ATT	AGT	AGT	GGN	GGT	AGT	TCC	ACC	TAC	TAT	CCA	GAC
	CGT	TGG	TAA	TCA	TCA	CCN	CCA	TCA	AGG	TGG	ATG	ATA	GGT	CTG
+1	S	V	K	G	R	F	T	I	S	R	D	N	A	K
253	AGT	GTG	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAT	GCC	AAG
	TCA	CAC	TTC	CCG	GCT	AAG	TGG	TAG	AGG	TCT	CTG	TTA	CGG	TTC
+1	N	T	L	Y	L	Q	M	S	S	L	R	S	E	D
295	AAC	ACC	CTG	TAC	CTG	CAA	ATG	AGC	AGT	CTG	AGG	TCT	GAG	GAC
	TTG	TGG	GAC	ATG	GAC	GTT	TAC	TCG	TCA	GAC	TCC	AGA	CTC	CTG
+1	T	A	M	Y	Y	C	T	R	E	G	G	G	F	T
337	ACA	GCC	ATG	TAT	TAC	TGT	ACA	AGA	GAG	GGG	GGT	GGT	TTC	ACC
	TGT	CGG	TAC	ATA	ATG	ACA	TGT	TCT	CTC	CCC	CCA	CCA	AAG	TGG
+1	V	N	W	Y	F	D	V	W	G	A	G	T	S	V
379	GTC	AAC	TGG	TAC	TTC	GAT	GTC	TGG	GGC	GCA	GGA	ACC	TCA	GTC
	CAG	TTG	ACC	ATG	AAG	CTA	CAG	ACC	CCG	CGT	CCT	TGG	AGT	CAG
Linker														
+1	T	V	S	S	G	G	G	S	G	G	R	A	S	
421	ACC	GTC	TCC	TCA	GGT	GGA	GGC	GGT	TCA	GGT	GGG	CGC	GCC	TCT
	TGG	CAG	AGG	AGT	CCA	CCT	CCG	CCA	AGT	CCA	CCC	GCG	CGG	AGA

Fig. 26-1

							VL							
+1	G	G	G	G	S	D	I	V	L	T	Q	S	P	A
463	GGC	GGT	GGC	GGA	TCG	GAC	ATT	GTG	CTG	ACA	CAG	TCT	CCA	GCT
	CCG	CCA	CCG	CCT	AGC	CTG	TAA	CAC	GAC	TGT	GTC	AGA	GGT	CGA
+1	S	L	A	V	S	L	G	Q	R	A	T	I	S	C
505	TCT	TTG	GCT	GTG	TCT	CTA	GGG	CAG	AGG	GCC	ACC	ATA	TCC	TGC
	AGA	AAC	CGA	CAC	AGA	GAT	CCC	GTC	TCC	CGG	TGG	TAT	AGG	ACG
+1	R	A	S	E	S	V	D	S	Y	G	Y	N	F	M
547	AGA	GCC	AGT	GAA	AGT	GTT	GAT	AGT	TAT	GGC	TAT	AAT	TTT	ATG
	TCT	CGG	TCA	CTT	TCA	CAA	CTA	TCA	ATA	CCG	ATA	TTA	AAA	TAC
+1	H	W	Y	Q	Q	I	P	G	Q	P	P	K	L	L
589	CAC	TGG	TAT	CAG	CAG	ATA	CCA	GGA	CAG	CCA	CCC	AAA	CTC	CTC
	GTG	ACC	ATA	GTC	GTC	TAT	GGT	CCT	GTC	GGT	GGG	TTT	GAG	GAG
+1	I	Y	R	A	S	N	L	E	S	G	I	P	A	R
631	ATC	TAT	CGT	GCA	TCC	AAC	CTA	GAG	TCT	GGG	ATC	CCT	GCC	AGG
	TAG	ATA	GCA	CGT	AGG	TTG	GAT	CTC	AGA	CCC	TAG	GGA	CGG	TCC
+1	F	S	G	S	G	S	R	T	D	F	T	L	T	I
673	TTC	AGT	GGC	AGT	GGG	TCT	AGG	ACA	GAC	TTC	ACC	CTC	ACC	ATT
	AAG	TCA	CCG	TCA	CCC	AGA	TCC	TGT	CTG	AAG	TGG	GAG	TGG	TAA
+1	N	P	V	E	A	D	D	V	A	T	Y	Y	C	Q
715	AAT	CCT	GTG	GAG	GCT	GAT	GAT	GTT	GCA	ACC	TAT	TAC	TGT	CAG
	TTA	GGA	CAC	CTC	CGA	CTA	CTA	CAA	CGT	TGG	ATA	ATG	ACA	GTC
+1	Q	S	N	E	D	P	L	T	F	G	T	G	T	R
757	CAA	AGT	AAT	GAG	GAT	CCG	CTC	ACG	TTC	GGT	ACT	GGG	ACC	AGA
	GTT	TCA	TTA	CTC	CTA	GGC	GAG	TGC	AAG	CCA	TGA	CCC	TGG	TCT
							Spacer				Alkaline phosphatase			
+1	L	E	I	K	R	A	A	A	A	R	A	P	E	M
799	CTG	GAA	ATA	AAA	CGG	GCG	GCC	GCA	GCC	CGG	GCA	CCA	GAA	ATG
	GAC	CTT	TAT	TTT	GCC	CGC	CGG	CGT	CGG	GCC	CGT	GGT	CTT	TAC
+1	P	V	L	E	N	R	A	A	Q	G	D	I	T	A
841	CCT	GTT	CTG	GAA	AAC	CGG	GCT	GCT	CAG	GGC	GAT	ATT	ACT	GCA
	GGA	CAA	GAC	CTT	TTG	GCC	CGA	CGA	GTC	CCG	CTA	TAA	TGA	CGT
+1	P	G	G	A	R	R	L	T	G	D	Q	T	A	A
883	CCC	GGC	GGT	GCT	CGC	CGT	TTA	ACG	GGT	GAT	CAG	ACT	GCC	GCT
	GGG	CCG	CCA	CGA	GCG	GCA	AAT	TGC	CCA	CTA	GTC	TGA	CGG	CGA
+1	L	R	D	S	L	S	D	K	P	A	K	N	I	I
925	CTG	CGT	GAT	TCT	CTT	AGC	GAT	AAA	CCT	GCA	AAA	AAT	ATT	ATT
	GAC	GCA	CTA	AGA	GAA	TCG	CTA	TTT	GGA	CGT	TTT	TTA	TAA	TAA

Fig. 26-2

+1	L	L	I	G	D	G	M	G	D	S	E	I	T	A
967	TTG	CTG	ATT	GGC	GAT	GGG	ATG	GGG	GAC	TCG	GAA	ATT	ACT	GCC
	AAC	GAC	TAA	CCG	CTA	CCC	TAC	CCC	CTG	AGC	CTT	TAA	TGA	CGG
+1	A	R	N	Y	A	E	G	A	G	G	F	F	K	G
1009	GCA	CGT	AAT	TAT	GCC	GAA	GGT	GCG	GGC	GGC	TTT	TTT	AAA	GGT
	CGT	GCA	TTA	ATA	CGG	CTT	CCA	CGC	CCG	CCG	AAA	AAA	TTT	CCA
+1	I	D	A	L	P	L	T	G	Q	Y	T	H	Y	A
1051	ATA	GAT	GCC	TTA	CCG	CTT	ACC	GGG	CAA	TAC	ACT	CAC	TAT	GCG
	TAT	CTA	CGG	AAT	GGC	GAA	TGG	CCC	GTT	ATG	TGA	GTG	ATA	CGC
+1	L	N	K	K	T	G	K	P	D	Y	V	T	D	S
1093	CTG	AAT	AAA	AAA	ACC	GGC	AAA	CCG	GAC	TAC	GTC	ACC	GAC	TCG
	GAC	TTA	TTT	TTT	TGG	CCG	TTT	GGC	CTG	ATG	CAG	TGG	CTG	AGC
+1	A	A	S	A	T	A	W	S	T	G	V	K	T	Y
1135	GCT	GCA	TCA	GCA	ACC	GCC	TGG	TCA	ACC	GGT	GTC	AAA	ACC	TAT
	CGA	CGT	AGT	CGT	TGG	CGG	ACC	AGT	TGG	CCA	CAG	TTT	TGG	ATA
+1	N	G	A	L	G	V	D	I	H	E	K	D	H	P
1177	AAC	GGC	GCG	CTG	GGC	GTC	GAT	ATT	CAC	GAA	AAA	GAT	CAC	CCA
	TTG	CCG	CGC	GAC	CCG	CAG	CTA	TAA	GTG	CTT	TTT	CTA	GTG	GGT
+1	T	I	L	E	M	A	K	A	A	G	L	A	T	G
1219	ACG	ATT	CTG	GAA	ATG	GCA	AAA	GCC	GCA	GGT	CTG	GCG	ACC	GGT
	TGC	TAA	GAC	CTT	TAC	CGT	TTT	CGG	CGT	CCA	GAC	CGC	TGG	CCA
+1	N	V	S	T	A	E	L	Q	D	A	T	P	A	A
1261	AAC	GTT	TCT	ACC	GCA	GAG	TTG	CAG	GAT	GCC	ACG	CCC	GCT	GCG
	TTG	CAA	AGA	TGG	CGT	CTC	AAC	GTC	CTA	CGG	TGC	GGG	CGA	CGC
+1	L	V	A	H	V	T	S	R	K	C	Y	G	P	S
1303	CTG	GTG	GCA	CAT	GTG	ACC	TCG	CGC	AAA	TGC	TAC	GGT	CCG	AGC
	GAC	CAC	CGT	GTA	CAC	TGG	AGC	GCG	TTT	ACG	ATG	CCA	GGC	TCG
+1	A	T	S	E	K	C	P	G	N	A	L	E	K	G
1345	GCG	ACC	AGT	GAA	AAA	TGT	CCG	GGT	AAC	GCT	CTG	GAA	AAA	GGC
	CGC	TGG	TCA	CTT	TTT	ACA	GGC	CCA	TTG	CGA	GAC	CTT	TTT	CCG
+1	G	K	G	S	I	T	E	Q	L	L	N	A	R	A
1387	GGA	AAA	GGA	TCG	ATT	ACC	GAA	CAG	CTG	CTT	AAC	GCT	CGT	GCC
	CCT	TTT	CCT	AGC	TAA	TGG	CTT	GTC	GAC	GAA	TTG	CGA	GCA	CGG
+1	D	V	T	L	G	G	G	A	K	T	F	A	E	T
1429	GAC	GTT	ACG	CTT	GGC	GGC	GGC	GCA	AAA	ACC	TTT	GCT	GAA	ACG
	CTG	CAA	TGC	GAA	CCG	CCG	CCG	CGT	TTT	TGG	AAA	CGA	CTT	TGC

Fig. 26-3

+1	A	T	A	G	E	W	Q	G	K	T	L	R	E	Q
1471	GCA	ACC	GCT	GGT	GAA	TGG	CAG	GGA	AAA	ACG	CTG	CGT	GAA	CAG
	CGT	TGG	CGA	CCA	CTT	ACC	GTC	CCT	TTT	TGC	GAC	GCA	CTT	GTC
+1	A	Q	A	R	G	Y	Q	L	V	S	D	A	A	S
1513	GCA	CAG	GCG	CGT	GGT	TAT	CAG	TTG	GTG	AGC	GAT	GCT	GCC	TCA
	CGT	GTC	CGC	GCA	CCA	ATA	GTC	AAC	CAC	TCG	CTA	CGA	CGG	AGT
+1	L	N	S	V	T	E	A	N	Q	Q	K	P	L	L
1555	CTG	AAT	TCG	GTG	ACG	GAA	GCG	AAT	CAG	CAA	AAA	CCC	CTG	CTT
	GAC	TTA	AGC	CAC	TGC	CTT	CGC	TTA	GTC	GTT	TTT	GGG	GAC	GAA
+1	G	L	F	A	D	G	N	M	P	V	R	W	L	G
1597	GGC	CTG	TTT	GCT	GAC	GGC	AAT	ATG	CCA	GTG	CGC	TGG	CTA	GGA
	CCG	GAC	AAA	CGA	CTG	CCG	TTA	TAC	GGT	CAC	GCG	ACC	GAT	CCT
+1	P	K	A	T	Y	H	G	N	I	D	K	P	A	V
1639	CCG	AAA	GCA	ACG	TAC	CAT	GGC	AAT	ATC	GAT	AAG	CCC	GCA	GTC
	GGC	TTT	CGT	TGC	ATG	GTA	CCG	TTA	TAG	CTA	TTC	GGG	CGT	CAG
+1	T	C	T	P	N	P	Q	R	N	D	S	V	P	T
1681	ACC	TGT	ACG	CCA	AAT	CCG	CAA	CGT	AAT	GAC	AGT	GTA	CCA	ACC
	TGG	ACA	TGC	GGT	TTA	GGC	GTT	GCA	TTA	CTG	TCA	CAT	GGT	TGG
+1	L	A	Q	M	T	D	K	A	I	E	L	L	S	K
1723	CTG	GCG	CAG	ATG	ACC	GAC	AAA	GCC	ATT	GAA	TTG	TTG	AGT	AAA
	GAC	CGC	GTC	TAC	TGG	CTG	TTT	CGG	TAA	CTT	AAC	AAC	TCA	TTT
+1	N	E	K	G	F	F	L	Q	V	E	G	A	S	I
1765	AAT	GAG	AAA	GGC	TTT	TTC	CTG	CAA	GTT	GAA	GGT	GCG	TCA	ATC
	TTA	CTC	TTT	CCG	AAA	AAG	GAC	GTT	CAA	CTT	CCA	CGC	AGT	TAG
+1	D	K	Q	D	H	A	A	N	P	C	G	Q	I	G
1807	GAT	AAA	CAG	GAT	CAT	GCT	GCG	AAT	CCT	TGT	GGG	CAA	ATT	GGC
	CTA	TTT	GTC	CTA	GTA	CGA	CGC	TTA	GGA	ACA	CCC	GTT	TAA	CCG
+1	E	T	V	D	L	D	E	A	V	Q	R	A	L	E
1849	GAG	ACG	GTC	GAT	CTC	GAT	GAA	GCC	GTA	CAA	CGG	GCG	CTG	GAA
	CTC	TGC	CAG	CTA	GAG	CTA	CTT	CGG	CAT	GTT	GCC	CGC	GAC	CTT
+1	F	A	K	K	E	G	N	T	L	V	I	V	T	A
1891	TTC	GCT	AAA	AAG	GAG	GGT	AAC	ACG	CTG	GTC	ATA	GTC	ACC	GCT
	AAG	CGA	TTT	TTC	CTC	CCA	TTG	TGC	GAC	CAG	TAT	CAG	TGG	CGA
+1	D	H	A	H	A	S	Q	I	V	A	P	D	T	K
1933	GAT	CAC	GCC	CAC	GCC	AGC	CAG	ATT	GTT	GCG	CCG	GAT	ACC	AAA
	CTA	GTG	CGG	GTG	CGG	TCG	GTC	TAA	CAA	CGC	GGC	CTA	TGG	TTT
+1	A	P	G	L	T	Q	A	L	N	T	K	D	G	A
1975	GCT	CCG	GGC	CTC	ACC	CAG	GCG	CTA	AAT	ACC	AAA	GAT	GGC	GCA
	CGA	GGC	CCG	GAG	TGG	GTC	CGC	GAT	TTA	TGG	TTT	CTA	CCG	CGT

Fig. 26-4

	+1	V	M	V	M	S	Y	G	N	S	E	E	D	S	Q	
2017		GTG	ATG	GTG	ATG	AGT	TAC	GGG	AAC	TCC	GAA	GAG	GAT	TCA	CAA	
		CAC	TAC	CAC	TAC	TCA	ATG	CCC	TTG	AGG	CTT	CTC	CTA	AGT	GTT	
	+1	E	H	T	G	S	Q	L	R	I	A	A	Y	G	P	
2059		GAA	CAT	ACC	GGC	AGT	CAG	TTG	CGT	ATT	GCG	GCG	TAT	GGC	CCG	
		CTT	GTA	TGG	CCG	TCA	GTC	AAC	GCA	TAA	CGC	CGC	ATA	CCG	GGC	
	+1	H	A	A	N	V	V	G	L	T	D	Q	T	D	L	
2101		CAT	GCC	GCC	AAT	GTT	GTT	GGA	CTG	ACC	GAC	CAG	ACC	GAT	CTC	
		GTA	CGG	CGG	TTA	CAA	CAA	CCT	GAC	TGG	CTG	GTC	TGG	CTA	GAG	
	+1	F	Y	T	M	K	A	A	L	G	D	I	His tag			
2143		TTC	TAC	ACC	ATG	AAA	GCC	GCT	CTG	GGG	GAT	ATC	A	H	H	
		AAG	ATG	TGG	TAC	TTT	CGG	CGA	GAC	CCC	CTA	TAG	GCA	CAC	CAT	
													CGT	GTG	GTA	
	+1	H	H	H	H	*										
2185		CAC	CAT	CAC	CAT	TAA										
		GTG	GTA	GTG	GTA	ATT										

Fig. 26-5

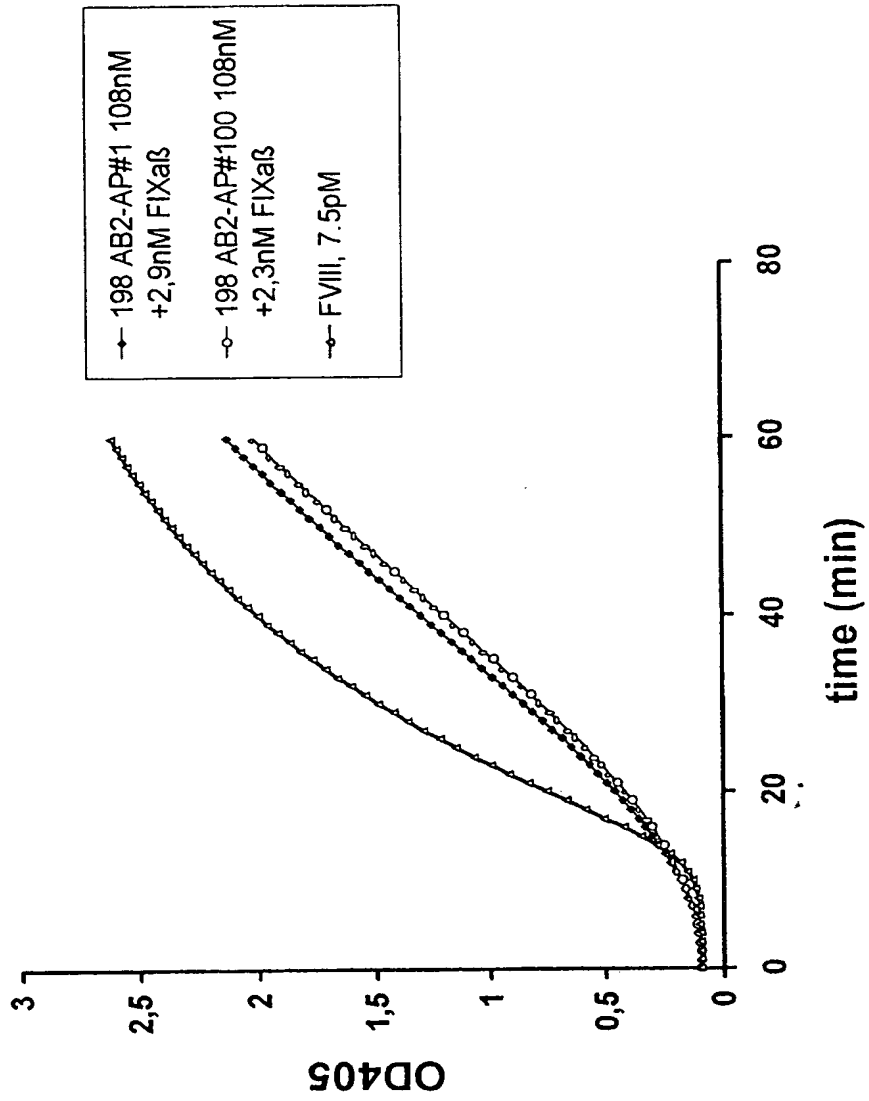


Fig. 27

PelB-Leader

+1	M	K	Y	L	L	P	T	A	A	A	G	L	L	L	L
1	ATG	AAA	TAC	CTA	TTG	CCT	ACG	GCA	GCC	GCT	GGA	TTG	TTA	TTA	CTC
	TAC	TTT	ATG	GAT	AAC	GGA	TGC	CGT	CGG	CGA	CCT	AAC	AAT	AAT	GAG

VH

+1	A	A	Q	P	A	M	A	E	V	K	L	V	E	S	G
46	GCG	GCC	CAG	CCG	GCC	ATG	GCG	GAG	GTG	AAG	CTG	GTG	GAG	TCT	GGG
	CGC	CGG	GTC	GGC	CGG	TAC	CGC	CTC	CAC	TTC	GAC	CAC	CTC	AGA	CCC

+1	G	G	L	V	K	P	G	G	S	L	K	L	S	C	A
91	GGA	GGC	TTA	GTG	AAG	CCT	GGA	GGG	TCC	CTG	AAA	CTC	TCC	TGT	GCA
	CCT	CCG	AAT	CAC	TTC	GGA	CCT	CCC	AGG	GAC	TTT	GAG	AGG	ACA	CGT

+1	A	S	G	F	T	F	S	S	Y	T	M	S	W	V	R
136	GCC	TCT	GGA	TTC	ACT	TTC	AGT	AGC	TAT	ACC	ATG	TCT	TGG	GTT	CGC
	CGG	AGA	CCT	AAG	TGA	AAG	TCA	TCG	ATA	TGG	TAC	AGA	ACC	CAA	GCG

+1	Q	T	P	E	K	R	L	E	W	V	A	T	I	S	S
181	CAG	ACT	CCG	GAG	AAG	AGG	CTG	GAG	TGG	GTC	GCA	ACC	ATT	AGT	AGT
	GTC	TGA	GGC	CTC	TTC	TCC	GAC	CTC	ACC	CAG	CGT	TGG	TAA	TCA	TCA

+1	G	G	S	S	T	Y	Y	P	D	S	V	K	G	R	F
226	GGN	GGT	AGT	TCC	ACC	TAC	TAT	CCA	GAC	AGT	GTG	AAG	GGC	CGA	TTC
	CCN	CCA	TCA	AGG	TGG	ATG	ATA	GGT	CTG	TCA	CAC	TTC	CCG	GCT	AAG

+1	T	I	S	R	D	N	A	K	N	T	L	Y	L	Q	M
271	ACC	ATC	TCC	AGA	GAC	AAT	GCC	AAG	AAC	ACC	CTG	TAC	CTG	CAA	ATG
	TGG	TAG	AGG	TCT	CTG	TTA	CGG	TTC	TTG	TGG	GAC	ATG	GAC	GTT	TAC

+1	S	S	L	R	S	E	D	T	A	M	Y	Y	C	T	R
316	AGC	AGT	CTG	AGG	TCT	GAG	GAC	ACA	GCC	ATG	TAT	TAC	TGT	ACA	AGA
	TCG	TCA	GAC	TCC	AGA	CTC	CTG	TGT	CGG	TAC	ATA	ATG	ACA	TGT	TCT

+1	E	G	G	G	F	T	V	N	W	Y	F	D	V	W	G
361	GAG	GGG	GGT	GGT	TTC	ACC	GTC	AAC	TGG	TAC	TTC	GAT	GTC	TGG	GGC
	CTC	CCC	CCA	CCA	AAG	TGG	CAG	TTG	ACC	ATG	AAG	CTA	CAG	ACC	CCG

Linker

+1	A	G	T	S	V	T	V	S	S	G	G	G	G	S	G
406	GCA	GGA	ACC	TCA	GTC	ACC	GTC	TCC	TCA	GGT	GGA	GGC	GGT	TCA	GGT
	CGT	CCT	TGG	AGT	CAG	TGG	CAG	AGG	AGT	CCA	CCT	CCG	CCA	AGT	CCA

VL

+1	G	R	A	S	G	G	G	G	S	D	I	V	L	T	Q
451	GGG	CGC	GCC	TCT	GGC	GGT	GGC	GGA	TCG	GAC	ATT	GTG	CTG	ACA	CAG
	CCC	GCG	CGG	AGA	CCG	CCA	CCG	CCT	AGC	CTG	TAA	CAC	GAC	TGT	GTC

Fig. 2P-1


```

+1  X   P   A   S   L   A   V   S   L   G   Q   R   A   T   I
496  TNT CCA GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG GCC ACC ATA
    ANA GGT CGA AGA AAC CGA CAC AGA GAT CCC GTC TCC CGG TGG TAT

+1  S   C   R   A   S   E   S   V   D   S   Y   G   Y   N   F
541  TCN TGC AGA GCC AGT GAA AGT GTT GAT AGT TAT GGC TAT AAT TTT
    AGN ACG TCT CGG TCA CTT TCA CAA CTA TCA ATA CCG ATA TTA AAA

+1  M   H   W   Y   Q   Q   I   P   G   Q   P   P   K   L   L
586  ATG CAC TGG TAT CAG CAG ATA CCA GGA CAG CCA CCC AAA CTC CTC
    TAC GTG ACC ATA GTC GTC TAT GGT CCT GTC GGT GGG TTT GAG GAG

+1  I   Y   R   A   S   N   L   E   S   G   I   P   A   R   F
631  ATC TAT CGT GCA TCC AAC CTA GAG TCT GGG ATC CCT GCC AGG TTC
    TAG ATA GCA CGT AGG TTG GAT CTC AGA CCC TAG GGA CGG TCC AAG

+1  S   G   S   G   S   R   T   D   F   T   L   T   I   N   P
676  AGT GGC AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC ATT AAT CCT
    TCA CCG TCA CCC AGA TCC TGT CTG AAG TGG GAG TGG TAA TTA GGA

+1  V   E   A   D   D   V   A   T   Y   Y   C   Q   Q   S   N
721  GTG GAG GCT GAT GAT GTT GCA ACC TAT TAC TGT CAG CAA AGT AAT
    CAC CTC CGA CTA CTA CAA CGT TGG ATA ATG ACA GTC GTT TCA TTA

+1  E   D   P   L   T   F   G   T   G   T   R   L   E   I   K
766  GAG GAT CCG CTC ACG TTC GGT ACT GGG ACC AGA CTG GAA ATA AAA
    CTC CTA GGC GAG TGC AAG CCA TGA CCC TGG TCT GAC CTT TAT TTT

          Spacer          Hinge                                Helix

+1  R   A   A   A   P   K   P   S   T   P   P   G   S   S   R
811  CGG GCG GCC GCA CCG AAG CCT TCC ACT CCG CCC GGG TCT TCC CGT
    GCC CGC CGG CGT GGC TTC GGA AGG TGA GGC GGG CCC AGA AGG GCA

+1  M   K   Q   L   E   D   K   V   E   E   L   L   S   K   N
856  ATG AAA CAG CTG GAA GAC AAA GTA GAG GAG CTC CTT AGC AAG AAC
    TAC TTT GTC GAC CTT CTG TTT CAT CTC CTC GAG GAA TCG TTC TTG

+1  Y   H   L   E   N   E   V   A   R   L   K   K   L   V   G
901  TAC CAT CTA GAA AAC GAG GTA GCT CGT CTG AAA AAG CTT GTT GGT
    ATG GTA GAT CTT TTG CTC CAT CGA GCA GAC TTT TTC GAA CAA CCA

          Spacer          His-tag

+1  E   R   G   G   H   H   H   H   H   *
946  GAA CGT GGT GGT CAC CAT CAC CAT CAC CAT TAA
    CTT GCA CCA CCA GTG GTA GTG GTA GTG GTA ATT

```

Fig. 28-2

PelB-leader

+1	M	K	Y	L	L	P	T	A	A	A	G	L	L	L
1	ATG	AAA	TAC	CTA	TTG	CCT	ACG	GCA	GCC	GCT	GGA	TTG	TTA	TTA
	TAC	TTT	ATG	GAT	AAC	GGA	TGC	CGT	CGG	CGA	CCT	AAC	AAT	AAT

										VH				
+1	L	A	A	Q	P	A	M	A	E	V	Q	L	Q	Q
43	CTC	GCG	GCC	CAG	CCG	GCC	ATG	GCC	GAG	GTT	CAG	CTT	CAG	CAG
	GAG	CGC	CGG	GTC	GGC	CGG	TAC	CGG	CTC	CAA	GTC	GAA	GTC	GTC

+1	S	G	P	E	L	V	K	P	G	A	S	V	K	I
85	TCT	GGA	CCT	GAG	CTG	GTG	AAG	CCC	GGG	GCC	TCA	GTG	AAG	ATT
	AGA	CCT	GGA	CTC	GAC	CAC	TTC	GGG	CCC	CGG	AGT	CAC	TTC	TAA

+1	S	C	K	A	S	G	Y	A	F	S	S	S	W	M
127	TCC	TGC	AAA	GCT	TCT	GGC	TAC	GCA	TTC	AGT	AGC	TCT	TGG	ATG
	AGG	ACG	TTT	CGA	AGA	CCG	ATG	CGT	AAG	TCA	TCG	AGA	ACC	TAC

+1	N	W	V	K	Q	R	P	G	Q	G	L	E	W	I
169	AAC	TGG	GTG	AAG	CAG	AGG	CCT	GGA	CAG	GGT	CTT	GAG	TGG	ATT
	TTG	ACC	CAC	TTC	GTC	TCC	GGA	CCT	GTC	CCA	GAA	CTC	ACC	TAA

+1	G	R	I	Y	P	G	N	G	D	T	N	Y	N	G
211	GGA	CGG	ATT	TAT	CCT	GGA	AAT	GGA	GAT	ACT	AAC	TAC	AAT	GGG
	CCT	GCC	TAA	ATA	GGA	CCT	TTA	CCT	CTA	TGA	TTG	ATG	TTA	CCC

+1	K	F	K	G	K	A	T	L	T	A	D	K	S	S
253	AAG	TTC	AAG	GGC	AAG	GCC	ACA	CTG	ACT	GCA	GAC	AAA	TCC	TCC
	TTC	AAG	TTC	CCG	TTC	CGG	TGT	GAC	TGA	CGT	CTG	TTT	AGG	AGG

+1	S	T	A	Y	M	Q	L	S	S	L	T	S	V	D
295	AGC	ACA	GCC	TAC	ATG	CAG	CTC	AGC	AGC	CTG	ACC	TCT	GTG	GAC
	TCG	TGT	CGG	ATG	TAC	GTC	GAG	TCG	TCG	GAC	TGG	AGA	CAC	CTG

+1	S	A	V	Y	F	C	A	D	G	N	V	Y	Y	Y
337	TCT	GCG	GTC	TAT	TTC	TGT	GCA	GAT	GGT	AAC	GTA	TAT	TAC	TAT
	AGA	CGC	CAG	ATA	AAG	ACA	CGT	CTA	CCA	TTG	CAT	ATA	ATG	ATA

+1	A	M	D	Y	W	G	Q	G	T	S	V	T	V	S
379	GCT	ATG	GAC	TAC	TGG	GGT	CAA	GGA	ACC	TCA	GTC	ACC	GTC	TCC
	CGA	TAC	CTG	ATG	ACC	CCA	GTT	CCT	TGG	AGT	CAG	TGG	CAG	AGG

										Linker				
+1	S	G	G	G	S	G	G	R	A	S	G	G	G	
421	TCA	GGT	GGA	GGC	GGT	TCA	GGT	GGG	CGC	GCC	TCT	GGC	GGT	GGC
	AGT	CCA	CCT	CCG	CCA	AGT	CCA	CCC	GCG	CGG	AGA	CCG	CCA	CCG

+1	G	S	Q	I	V	L	T	Q	S	P	A	S	L	A
463	GGA	TCG	CAA	ATT	GTT	CTC	ACC	CAG	TCT	CCT	GCT	TCC	TTA	GCT
	CCT	AGC	GTT	TAA	CAA	GAG	TGG	GTC	AGA	GGA	CGA	AGG	AAT	CGA

Fig. 29-1

Fig. 29-2

```

+1   Y   A   E   G   A   G   G   F   F   K   G   I   D   A
1009 TAT GCC GAA GGT GCG GGC GGC TTT TTT AAA GGT ATA GAT GCC
     ATA CGG CTT CCA CGC CCG CCG AAA AAA TTT CCA TAT CTA CGG

+1   L   P   L   T   G   Q   Y   T   H   Y   A   L   N   K
1051 TTA CCG CTT ACC GGG CAA TAC ACT CAC TAT GCG CTG AAT AAA
     AAT GGC GAA TGG CCC GTT ATG TGA GTG ATA CGC GAC TTA TTT

+1   K   T   G   K   P   D   Y   V   T   D   S   A   A   S
1093 AAA ACC GGC AAA CCG GAC TAC GTC ACC GAC TCG GCT GCA TCA
     TTT TGG CCG TTT GGC CTG ATG CAG TGG CTG AGC CGA CGT AGT

+1   A   T   A   W   S   T   G   V   K   T   Y   N   G   A
1135 GCA ACC GCC TGG TCA ACC GGT GTC AAA ACC TAT AAC GGC GCG
     CGT TGG CGG ACC AGT TGG CCA CAG TTT TGG ATA TTG CCG CGC

+1   L   G   V   D   I   H   E   K   D   H   P   T   I   L
1177 CTG GGC GTC GAT ATT CAC GAA AAA GAT CAC CCA ACG ATT CTG
     GAC CCG CAG CTA TAA GTG CTT TTT CTA GTG GGT TGC TAA GAC

+1   E   M   A   K   A   A   G   L   A   T   G   N   V   S
1219 GAA ATG GCA AAA GCC GCA GGT CTG GCG ACC GGT AAC GTT TCT
     CTT TAC CGT TTT CGG CGT CCA GAC CGC TGG CCA TTG CAA AGA

+1   T   A   E   L   Q   D   A   T   P   A   A   L   V   A
1261 ACC GCA GAG TTG CAG GAT GCC ACG CCC GCT GCG CTG GTG GCA
     TGG CGT CTC AAC GTC CTA CGG TGC GGG CGA CGC GAC CAC CGT

+1   H   V   T   S   R   K   C   Y   G   P   S   A   T   S
1303 CAT GTG ACC TCG CGC AAA TGC TAC GGT CCG AGC GCG ACC AGT
     GTA CAC TGG AGC GCG TTT ACG ATG CCA GGC TCG CGC TGG TCA

+1   E   K   C   P   G   N   A   L   E   K   G   G   K   G
1345 GAA AAA TGT CCG GGT AAC GCT CTG GAA AAA GGC GGA AAA GGA
     CTT TTT ACA GGC CCA TTG CGA GAC CTT TTT CCG CCT TTT CCT

+1   S   I   T   E   Q   L   L   N   A   R   A   D   V   T
1387 TCG ATT ACC GAA CAG CTG CTT AAC GCT CGT GCC GAC GTT ACG
     AGC TAA TGG CTT GTC GAC GAA TTG CGA GCA CGG CTG CAA TGC

+1   L   G   G   G   A   K   T   F   A   E   T   A   T   A
1429 CTT GGC GGC GGC GCA AAA ACC TTT GCT GAA ACG GCA ACC GCT
     GAA CCG CCG CCG CGT TTT TGG AAA CGA CTT TGC CGT TGG CGA

+1   G   E   W   Q   G   K   T   L   R   E   Q   A   Q   A
1471 GGT GAA TGG CAG GGA AAA ACG CTG CGT GAA CAG GCA CAG GCG
     CCA CTT ACC GTC CCT TTT TGC GAC GCA CTT GTC CGT GTC CGC

```

Fig. 29-3

+1	R	G	Y	Q	L	V	S	D	A	A	S	L	N	S
1513	CGT	GGT	TAT	CAG	TTG	GTG	AGC	GAT	GCT	GCC	TCA	CTG	AAT	TCG
	GCA	CCA	ATA	GTC	AAC	CAC	TCG	CTA	CGA	CGG	AGT	GAC	TTA	AGC
+1	V	T	E	A	N	Q	Q	K	P	L	L	G	L	F
1555	GTG	ACG	GAA	GCG	AAT	CAG	CAA	AAA	CCC	CTG	CTT	GGC	CTG	TTT
	CAC	TGC	CTT	CGC	TTA	GTC	GTT	TTT	GGG	GAC	GAA	CCG	GAC	AAA
+1	A	D	G	N	M	P	V	R	W	L	G	P	K	A
1597	GCT	GAC	GGC	AAT	ATG	CCA	GTG	CGC	TGG	CTA	GGA	CCG	AAA	GCA
	CGA	CTG	CCG	TTA	TAC	GGT	CAC	GCG	ACC	GAT	CCT	GGC	TTT	CGT
+1	T	Y	H	G	N	I	D	K	P	A	V	T	C	T
1639	ACG	TAC	CAT	GGC	AAT	ATC	GAT	AAG	CCC	GCA	GTC	ACC	TGT	ACG
	TGC	ATG	GTA	CCG	TTA	TAG	CTA	TTC	GGG	CGT	CAG	TGG	ACA	TGC
+1	P	N	P	Q	R	N	D	S	V	P	T	L	A	Q
1681	CCA	AAT	CCG	CAA	CGT	AAT	GAC	AGT	GTA	CCA	ACC	CTG	GCG	CAG
	GGT	TTA	GGC	GTT	GCA	TTA	CTG	TCA	CAT	GGT	TGG	GAC	CGC	GTC
+1	M	T	D	K	A	I	E	L	L	S	K	N	E	K
1723	ATG	ACC	GAC	AAA	GCC	ATT	GAA	TTG	TTG	AGT	AAA	AAT	GAG	AAA
	TAC	TGG	CTG	TTT	CGG	TAA	CTT	AAC	AAC	TCA	TTT	TTA	CTC	TTT
+1	G	F	F	L	Q	V	E	G	A	S	I	D	K	Q
1765	GGC	TTT	TTC	CTG	CAA	GTT	GAA	GGT	GCG	TCA	ATC	GAT	AAA	CAG
	CCG	AAA	AAG	GAC	GTT	CAA	CTT	CCA	CGC	AGT	TAG	CTA	TTT	GTC
+1	D	H	A	A	N	P	C	G	Q	I	G	E	T	V
1807	GAT	CAT	GCT	GCG	AAT	CCT	TGT	GGG	CAA	ATT	GGC	GAG	ACG	GTC
	CTA	GTA	CGA	CGC	TTA	GGA	ACA	CCC	GTT	TAA	CCG	CTC	TGC	CAG
+1	D	L	D	E	A	V	Q	R	A	L	E	F	A	K
1849	GAT	CTC	GAT	GAA	GCC	GTA	CAA	CGG	GCG	CTG	GAA	TTC	GCT	AAA
	CTA	GAG	CTA	CTT	CGG	CAT	GTT	GCC	CGC	GAC	CTT	AAG	CGA	TTT
+1	K	E	G	N	T	L	V	I	V	T	A	D	H	A
1891	AAG	GAG	GGT	AAC	ACG	CTG	GTC	ATA	GTC	ACC	GCT	GAT	CAC	GCC
	TTC	CTC	CCA	TTG	TGC	GAC	CAG	TAT	CAG	TGG	CGA	CTA	GTG	CGG
+1	H	A	S	Q	I	V	A	P	D	T	K	A	P	G
1933	CAC	GCC	AGC	CAG	ATT	GTT	GCG	CCG	GAT	ACC	AAA	GCT	CCG	GGC
	GTG	CGG	TCG	GTC	TAA	CAA	CGC	GGC	CTA	TGG	TTT	CGA	GGC	CCG
+1	L	T	Q	A	L	N	T	K	D	G	A	V	M	V
1975	CTC	ACC	CAG	GCG	CTA	AAT	ACC	AAA	GAT	GGC	GCA	GTG	ATG	GTG
	GAG	TGG	GTC	CGC	GAT	TTA	TGG	TTT	CTA	CCG	CGT	CAC	TAC	CAC

Fig. 29-4

	+1	M	S	Y	G	N	S	E	E	D	S	Q	E	H	T
2017		ATG	AGT	TAC	GGG	AAC	TCC	GAA	GAG	GAT	TCA	CAA	GAA	CAT	ACC
		TAC	TCA	ATG	CCC	TTG	AGG	CTT	CTC	CTA	AGT	GTT	CTT	GTA	TGG
	+1	G	S	Q	L	R	I	A	A	Y	G	P	H	A	A
2059		GGC	AGT	CAG	TTG	CGT	ATT	GCG	GCG	TAT	GGC	CCG	CAT	GCC	GCC
		CCG	TCA	GTC	AAC	GCA	TAA	CGC	CGC	ATA	CCG	GGC	GTA	CGG	CGG
	+1	N	V	V	G	L	T	D	Q	T	D	L	F	Y	T
2101		AAT	GTT	GTT	GGA	CTG	ACC	GAC	CAG	ACC	GAT	CTC	TTC	TAC	ACC
		TTA	CAA	CAA	CCT	GAC	TGG	CTG	GTC	TGG	CTA	GAG	AAG	ATG	TGG
	+1	M	K	A	A	L	G	D	I	A	His tag				
2143		ATG	AAA	GCC	GCT	CTG	GGG	GAT	ATC	GCA	CAC	CAT	CAC	CAT	CAC
		TAC	TTT	CGG	CGA	GAC	CCC	CTA	TAG	CGT	GTG	GTA	GTG	GTA	GTG
	+1	H	*												
2185		CAT	TAA												
		GTA	ATT												

Fig. 29-5

PelB-Leader

+1	M	K	Y	L	L	P	T	A	A	A	G	L	L	L	L
1	ATG	AAA	TAC	CTA	TTG	CCT	ACG	GCA	GCC	GCT	GGA	TTG	TTA	TTA	CTC
	TAC	TTT	ATG	GAT	AAC	GGA	TGC	CGT	CGG	CGA	CCT	AAC	AAT	AAT	GAG

+1	A	A	Q	P	A	M	A	VH							
46	GCG	GCC	CAG	CCG	GCC	ATG	GCG	GAG	GTT	CAG	CTT	CAG	CAG	TCT	GGA
	CGC	CGG	GTC	GGC	CGG	TAC	CGC	CTC	CAA	GTC	GAA	GTC	GTC	AGA	CCT

+1	P	E	L	V	K	P	G	A	S	V	K	I	S	C	K
91	CCT	GAG	CTG	GTG	AAG	CCC	GGG	GCC	TCA	GTG	AAG	ATT	TCC	TGC	AAA
	GGA	CTC	GAC	CAC	TTC	GGG	CCC	CGG	AGT	CAC	TTC	TAA	AGG	ACG	TTT

+1	A	S	G	Y	A	F	S	S	S	W	M	N	W	V	K
136	GCT	TCT	GGC	TAC	GCA	TTC	AGT	AGC	TCT	TGG	ATG	AAC	TGG	GTG	AAG
	CGA	AGA	CCG	ATG	CGT	AAG	TCA	TCG	AGA	ACC	TAC	TTG	ACC	CAC	TTC

+1	Q	R	P	G	Q	G	L	E	W	I	G	R	I	Y	P
181	CAG	AGG	CCT	GGA	CAG	GGT	CTT	GAG	TGG	ATT	GGA	CGG	ATT	TAT	CCT
	GTC	TCC	GGA	CCT	GTC	CCA	GAA	CTC	ACC	TAA	CCT	GCC	TAA	ATA	GGA

+1	G	N	G	D	T	N	Y	N	G	K	F	K	G	K	A
226	GGA	AAT	GGA	GAT	ACT	AAC	TAC	AAT	GGG	AAG	TTC	AAG	GGC	AAG	GCC
	CCT	TTA	CCT	CTA	TGA	TTG	ATG	TTA	CCC	TTC	AAG	TTC	CCG	TTC	CGG

+1	T	L	T	A	D	K	S	S	S	T	A	Y	M	Q	L
271	ACA	CTG	ACT	GCA	GAC	AAA	TCC	TCC	AGC	ACA	GCC	TAC	ATG	CAG	CTC
	TGT	GAC	TGA	CGT	CTG	TTT	AGG	AGG	TCG	TGT	CGG	ATG	TAC	GTC	GAG

+1	S	S	L	T	S	V	D	S	A	V	Y	F	C	A	D
316	AGC	AGC	CTG	ACC	TCT	GTG	GAC	TCT	GCG	GTC	TAT	TTC	TGT	GCA	GAT
	TCG	TCG	GAC	TGG	AGA	CAC	CTG	AGA	CGC	CAG	ATA	AAG	ACA	CGT	CTA

+1	G	N	V	Y	Y	Y	A	M	D	Y	W	G	Q	G	T
361	GGT	AAC	GTA	TAT	TAC	TAT	GCT	ATG	GAC	TAC	TGG	GGT	CAA	GGA	ACC
	CCA	TTG	CAT	ATA	ATG	ATA	CGA	TAC	CTG	ATG	ACC	CCA	GTT	CCT	TGG

+1	S	V	T	V	S	S	Linker								
406	TCA	GTC	ACC	GTC	TCC	TCA	GGT	GGA	GGC	GGT	TCA	GGT	GGG	CGC	GCC
	AGT	CAG	TGG	CAG	AGG	AGT	CCA	CCT	CCG	CCA	AGT	CCA	CCC	GCG	CGG

Fig. 30-1

Fig. 30-2

Spacer		His-tag						
+1	G	H	H	H	H	H	H	*
946	GGT	CAC	CAT	CAC	CAT	CAC	CAT	TAA
	CCA	GTG	GTA	GTG	GTA	GTG	GTA	ATT

Fig. 30-3

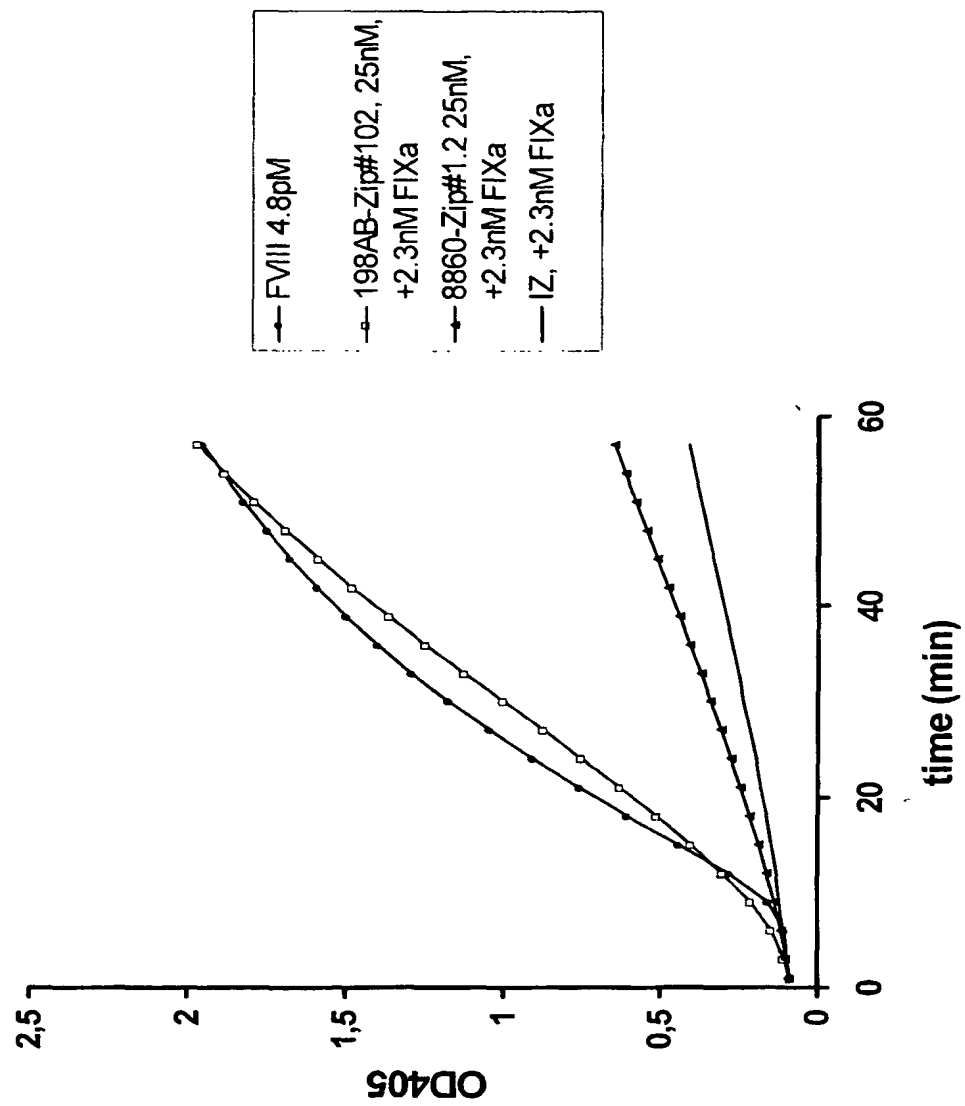


Fig. 31

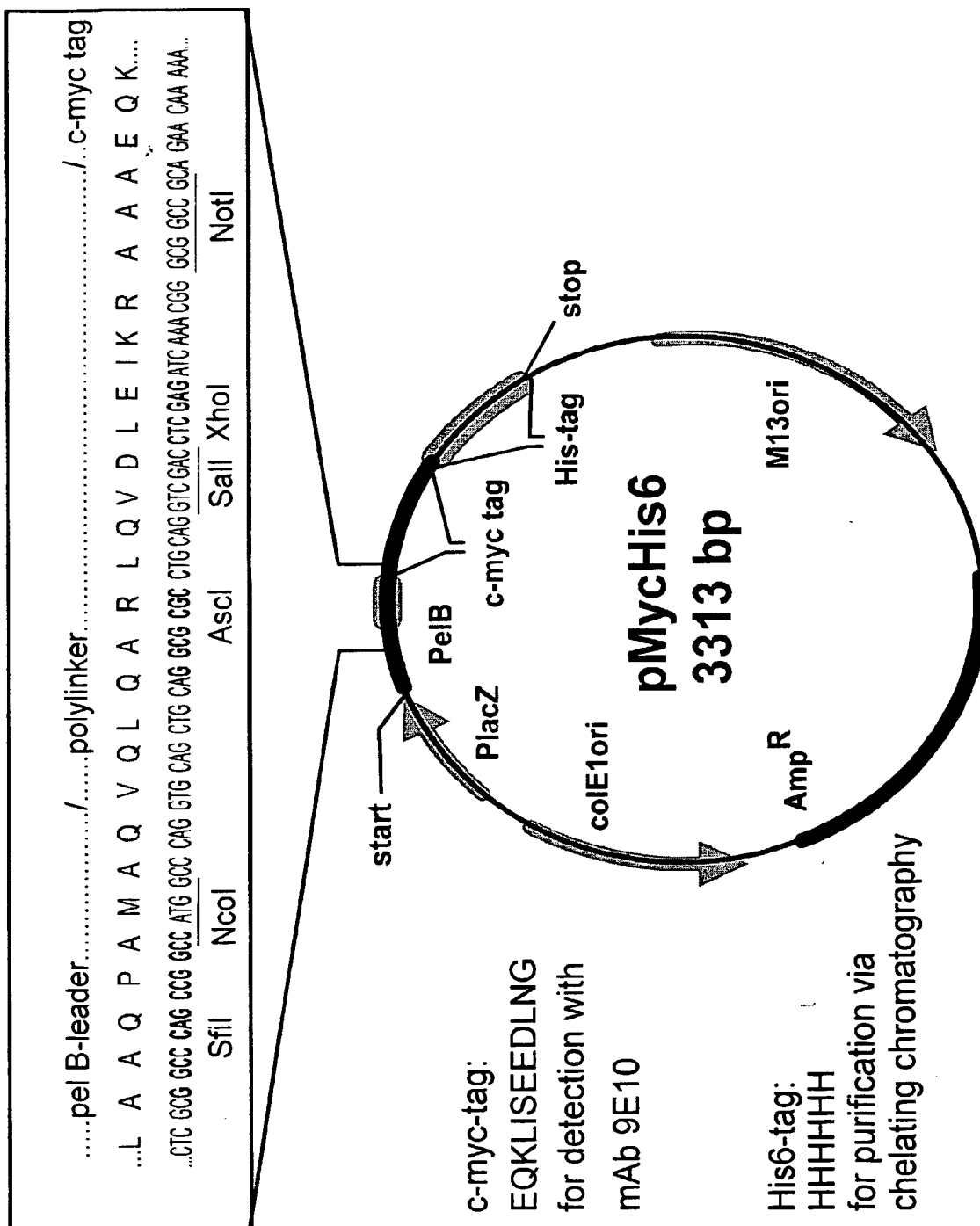


Fig. 32

HindIII
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2206 CAG GAA ACA GCT ATG ACC ATG ATT ACG CCA AGC TTC CAT GAA AAT  
GTC CTT TGT CGA TAC TGG TAC TAA TGC GGT TCG AAG GTA CTT TTA

PelB-Leader  
M K Y L L P T

2251 TCT ATT TCA AGG AGA CAG TCA TAA TGA AAT ACC TAT TGC CTA CGG  
AGA TAA AGT TCC TCT GTC AGT ATT ACT TTA TGG ATA ACG GAT GCC

A A A G L L L L A A Q P A M A

*SfiI*  
~~~~~

2296 CAG CCG CTG GAT TGT TAT TAC TCG CGG CCC AGC CGG CCA TGG CCC
GTC GGC GAC CTA ACA ATA ATG AGC GCC GGG TCG GCC GGT ACC GGG

Polylinker
Q V Q L Q A R L Q V D L E I K

AscI
~~~~~

2341 AGG TGC AGC TGC AGG CGC GCC TGC AGG TCG ACC TCG AGA TCA AAC  
TCC ACG TCG ACG TCC GCG CGG ACG TCC AGC TGG AGC TCT AGT TTG

Spacer Myc-tag  
R A A A E Q K L I S E E D L N

*NotI*  
~~~~~

2386 GGG CGG CCG CAG AAC AAA AAC TCA TCT CAG AAG AGG ATC TGA ATG
CCC GCC GGC GTC TTG TTT TTG AGT AGA GTC TTC TCC TAG ACT TAC

Spacer His tag
G A A H H H H H * *

EcoRI
~~~~~

2431 GGG CGG CAC ATC ACC ATC ACC ATC ACT AAT AAG AAT TCA CTG GCC  
CCC GCC GTG TAG TGG TAG TGG TAG TGA TTA TTC TTA AGT GAC CGG

Fig. 33

| PelB-leader |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| +1          | M   | K   | Y   | L   | L   | P   | T   | A   | A   | A   | G   | L   | L   | L   | L   |
| 1           | ATG | AAA | TAC | CTA | TTG | CCT | ACG | GCA | GCC | GCT | GGA | TTG | TTA | TTA | CTC |
|             | TAC | TTT | ATG | GAT | AAC | GGA | TGC | CGT | CGG | CGA | CCT | AAC | AAT | AAT | GAG |
| VH          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| +1          | A   | A   | Q   | P   | A   | M   | A   | E   | V   | K   | L   | V   | E   | S   | G   |
| 46          | GCG | GCC | CAG | CCG | GCC | ATG | GCC | GAG | GTG | AAG | CTG | GTG | GAG | TCT | GGG |
|             | CGC | CGG | GTC | GGC | CGG | TAC | CGG | CTC | CAC | TTC | GAC | CAC | CTC | AGA | CCC |
| +1          | G   | G   | L   | V   | K   | P   | G   | G   | S   | L   | K   | L   | S   | C   | A   |
| 91          | GGA | GGC | TTA | GTG | AAG | CCT | GGA | GGG | TCC | CTG | AAA | CTC | TCC | TGT | GCA |
|             | CCT | CCG | AAT | CAC | TTC | GGA | CCT | CCC | AGG | GAC | TTT | GAG | AGG | ACA | CGT |
| +1          | A   | S   | G   | F   | T   | F   | S   | S   | Y   | T   | M   | S   | W   | V   | R   |
| 136         | GCC | TCT | GGA | TTC | ACT | TTC | AGT | AGC | TAT | ACC | ATG | TCT | TGG | GTT | CGC |
|             | CGG | AGA | CCT | AAG | TGA | AAG | TCA | TCG | ATA | TGG | TAC | AGA | ACC | CAA | GCG |
| +1          | Q   | T   | P   | E   | K   | R   | L   | E   | W   | V   | A   | T   | I   | S   | S   |
| 181         | CAG | ACT | CCG | GAG | AAG | AGG | CTG | GAG | TGG | GTC | GCA | ACC | ATT | AGT | AGT |
|             | GTC | TGA | GGC | CTC | TTC | TCC | GAC | CTC | ACC | CAG | CGT | TGG | TAA | TCA | TCA |
| +1          | G   | G   | S   | S   | T   | Y   | Y   | P   | D   | S   | V   | K   | G   | R   | F   |
| 226         | GGN | GGT | AGT | TCC | ACC | TAC | TAT | CCA | GAC | AGT | GTG | AAG | GGC | CGA | TTC |
|             | CCN | CCA | TCA | AGG | TGG | ATG | ATA | GGT | CTG | TCA | CAC | TTC | CCG | GCT | AAG |
| +1          | T   | I   | S   | R   | D   | N   | A   | K   | N   | T   | L   | Y   | L   | Q   | M   |
| 271         | ACC | ATC | TCC | AGA | GAC | AAT | GCC | AAG | AAC | ACC | CTG | TAC | CTG | CAA | ATG |
|             | TGG | TAG | AGG | TCT | CTG | TTA | CGG | TTC | TTG | TGG | GAC | ATG | GAC | GTT | TAC |
| +1          | S   | S   | L   | R   | S   | E   | D   | T   | A   | M   | Y   | Y   | C   | T   | R   |
| 316         | AGC | AGT | CTG | AGG | TCT | GAG | GAC | ACA | GCC | ATG | TAT | TAC | TGT | ACA | AGA |
|             | TCG | TCA | GAC | TCC | AGA | CTC | CTG | TGT | CGG | TAC | ATA | ATG | ACA | TGT | TCT |
| +1          | E   | G   | G   | G   | F   | T   | V   | N   | W   | Y   | F   | D   | V   | W   | G   |
| 361         | GAG | GGG | GGT | GGT | TTC | ACC | GTC | AAC | TGG | TAC | TTC | GAT | GTC | TGG | GGC |
|             | CTC | CCC | CCA | CCA | AAG | TGG | CAG | TTG | ACC | ATG | AAG | CTA | CAG | ACC | CCG |
| Leader      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| +1          | A   | G   | T   | S   | V   | T   | V   | S   | S   | G   | G   | G   | G   | S   | G   |
| 406         | GCA | GGA | ACC | TCA | GTC | ACC | GTC | TCC | TCA | GGT | GGA | GGC | GGT | TCA | GGT |
|             | CGT | CCT | TGG | AGT | CAG | TGG | CAG | AGG | AGT | CCA | CCT | CCG | CCA | AGT | CCA |
| VK          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| +1          | G   | R   | A   | S   | G   | G   | G   | G   | S   | D   | I   | V   | L   | T   | Q   |
| 451         | GGG | CGC | GCC | TCT | GGC | GGT | GGC | GGA | TCG | GAC | ATT | GTG | CTG | ACA | CAG |

Fig. 34-1

```

      CCC GCG CGG AGA CCG CCA CCG CCT AGC CTG TAA CAC GAC TGT GTC
+1   S   P   A   S   L   A   V   S   L   G   Q   R   A   T   I
496  TCT CCA GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG GCC ACC ATA
      AGA GGT CGA AGA AAC CGA CAC AGA GAT CCC GTC TCC CGG TGG TAT

+1   S   C   R   A   S   E   S   V   D   S   Y   G   Y   N   F
541  TCC TGC AGA GCC AGT GAA AGT GTT GAT AGT TAT GGC TAT AAT TTT
      AGG ACG TCT CGG TCA CTT TCA CAA CTA TCA ATA CCG ATA TTA AAA

+1   M   H   W   Y   Q   Q   I   P   G   Q   P   P   K   L   L
586  ATG CAC TGG TAT CAG CAG ATA CCA GGA CAG CCA CCC AAA CTC CTC
      TAC GTG ACC ATA GTC GTC TAT GGT CCT GTC GGT GGG TTT GAG GAG

+1   I   Y   R   A   S   N   L   E   S   G   I   P   A   R   F
631  ATC TAT CGT GCA TCC AAC CTA GAG TCT GGG ATC CCT GCC AGG TTC
      TAG ATA GCA CGT AGG TTG GAT CTC AGA CCC TAG GGA CGG TCC AAG

+1   S   G   S   G   S   R   T   D   F   T   L   T   I   N   P
676  AGT GGC AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC ATT AAT CCT
      TCA CCG TCA CCC AGA TCC TGT CTG AAG TGG GAG TGG TAA TTA GGA

+1   V   E   A   D   D   V   A   T   Y   Y   C   Q   Q   S   N
721  GTG GAG GCT GAT GAT GTT GCA ACC TAT TAC TGT CAG CAA AGT AAT
      CAC CTC CGA CTA CTA CAA CGT TGG ATA ATG ACA GTC GTT TCA TTA

+1   E   D   P   L   T   F   G   T   G   T   R   L   E   I   K
766  GAG GAT CCG CTC ACG TTC GGT ACT GGG ACC AGA CTG GAA ATA AAA
      CTC CTA GGC GAG TGC AAG CCA TGA CCC TGG TCT GAC CTT TAT TTT

+1   R   |   Spacer   |   Myc-tag
811  CGG | A   A   A   | E   Q   K   L   I   S   E   E   D   L   N
      GCC | GCG GCC GCA | GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT
          | CGC CGG CGT | CTT GTT TTT GAG TAG AGT CTT CTC CTA GAC TTA

+1   G   |   Spacer   |   His tag
856  GGG | A   A   | H   H   H   H   H   H   *   *
      CCC | GCG GCA | CAT CAC CAT CAC CAT CAC TAA TAA
          | CGC CGT | GTA GTG GTA GTG GTA GTG ATT ATT

```

Fig. 34-2

PelB-leader

|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|-----|
| +1  | M   | K   | Y   | L   | L   | P   | T   | A      | A   | A   | G   | L   | L   | L   | L   |
| 1   | ATG | AAA | TAC | CTA | TTG | CCT | ACG | GCA    | GCC | GCT | GGA | TTG | TTA | TTA | CTC |
|     | TAC | TTT | ATG | GAT | AAC | GGA | TGC | CGT    | CGG | CGA | CCT | AAC | AAT | AAT | GAG |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     | VH     |     |     |     |     |     |     |     |
| +1  | A   | A   | Q   | P   | A   | M   | A   | E      | V   | Q   | L   | Q   | Q   | S   | G   |
| 46  | GCG | GCC | CAG | CCG | GCC | ATG | GCC | GAG    | GTT | CAG | CTT | CAG | CAG | TCT | GGA |
|     | CGC | CGG | GTC | GGC | CGG | TAC | CGG | CTC    | CAA | GTC | GAA | GTC | GTC | AGA | CCT |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
| +1  | P   | E   | L   | V   | K   | P   | G   | A      | S   | V   | K   | I   | S   | C   | K   |
| 91  | CCT | GAG | CTG | GTG | AAG | CCC | GGG | GCC    | TCA | GTG | AAG | ATT | TCC | TGC | AAA |
|     | GGA | CTC | GAC | CAC | TTC | GGG | CCC | CGG    | AGT | CAC | TTC | TAA | AGG | ACG | TTT |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
| +1  | A   | S   | G   | Y   | A   | F   | S   | S      | S   | W   | M   | N   | W   | V   | K   |
| 136 | GCT | TCT | GGC | TAC | GCA | TTC | AGT | AGC    | TCT | TGG | ATG | AAC | TGG | GTG | AAG |
|     | CGA | AGA | CCG | ATG | CGT | AAG | TCA | TCG    | AGA | ACC | TAC | TTG | ACC | CAC | TTC |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
| +1  | Q   | R   | P   | G   | Q   | G   | L   | E      | W   | I   | G   | R   | I   | Y   | P   |
| 181 | CAG | AGG | CCT | GGA | CAG | GGT | CTT | GAG    | TGG | ATT | GGA | CGG | ATT | TAT | CCT |
|     | GTC | TCC | GGA | CCT | GTC | CCA | GAA | CTC    | ACC | TAA | CCT | GCC | TAA | ATA | GGA |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
| +1  | G   | N   | G   | D   | T   | N   | Y   | N      | G   | K   | F   | K   | G   | K   | A   |
| 226 | GGA | AAT | GGA | GAT | ACT | AAC | TAC | AAT    | GGG | AAG | TTC | AAG | GGC | AAG | GCC |
|     | CCT | TTA | CCT | CTA | TGA | TTG | ATG | TTA    | CCC | TTC | AAG | TTC | CCG | TTC | CGG |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
| +1  | T   | L   | T   | A   | D   | K   | S   | S      | S   | T   | A   | Y   | M   | Q   | L   |
| 271 | ACA | CTG | ACT | GCA | GAC | AAA | TCC | TCC    | AGC | ACA | GCC | TAC | ATG | CAG | CTC |
|     | TGT | GAC | TGA | CGT | CTG | TTT | AGG | AGG    | TCG | TGT | CGG | ATG | TAC | GTC | GAG |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
| +1  | S   | S   | L   | T   | S   | V   | D   | S      | A   | V   | Y   | F   | C   | A   | D   |
| 316 | AGC | AGC | CTG | ACC | TCT | GTG | GAC | TCT    | GCG | GTC | TAT | TTC | TGT | GCA | GAT |
|     | TCG | TCG | GAC | TGG | AGA | CAC | CTG | AGA    | CGC | CAG | ATA | AAG | ACA | CGT | CTA |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
| +1  | G   | N   | V   | Y   | Y   | Y   | A   | M      | D   | Y   | W   | G   | Q   | G   | T   |
| 361 | GGT | AAC | GTA | TAT | TAC | TAT | GCT | ATG    | GAC | TAC | TGG | GGT | CAA | GGA | ACC |
|     | CCA | TTG | CAT | ATA | ATG | ATA | CGA | TAC    | CTG | ATG | ACC | CCA | GTT | CCT | TGG |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     | Leader |     |     |     |     |     |     |     |
| +1  | S   | V   | T   | V   | S   | S   | G   | G      | G   | S   | G   | G   | R   | A   |     |
| 406 | TCA | GTC | ACC | GTC | TCC | TCA | GGT | GGA    | GGC | GGT | TCA | GGT | GGG | CGC | GCC |
|     | AGT | CAG | TGG | CAG | AGG | AGT | CCA | CCT    | CCG | CCA | AGT | CCA | CCC | GCG | CGG |
|     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     | VL     |     |     |     |     |     |     |     |
| +1  | S   | G   | G   | G   | G   | S   | Q   | I      | V   | L   | T   | Q   | S   | P   | A   |
| 451 | TCT | GGC | GGT | GGC | GGA | TCG | CAA | ATT    | GTT | CTC | ACC | CAG | TCT | CCT | GCT |
|     | AGA | CCG | CCA | CCG | CCT | AGC | GTT | TAA    | CAA | GAG | TGG | GTC | AGA | GGA | CGA |

Fig. 35-1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| +1  | S   | L   | A   | V   | S   | L   | G   | Q   | R   | A   | T   | I   | S   | C   | R   |
| 496 | TCC | TTA | GCT | GTA | TCT | CTG | GGG | CAG | AGG | GCC | ACC | ATC | TCA | TGC | AGG |
|     | AGG | AAT | CGA | CAT | AGA | GAC | CCC | GTC | TCC | CGG | TGG | TAG | AGT | ACG | TCC |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| +1  | A   | S   | K   | S   | V   | S   | T   | S   | G   | Y   | S   | Y   | M   | H   | W   |
| 541 | GCC | AGC | AAA | AGT | GTC | AGT | ACA | TCT | GGC | TAT | AGT | TAT | ATG | CAC | TGG |
|     | CGG | TCG | TTT | TCA | CAG | TCA | TGT | AGA | CCG | ATA | TCA | ATA | TAC | GTG | ACC |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| +1  | Y   | Q   | Q   | K   | P   | G   | Q   | P   | P   | K   | L   | L   | I   | Y   | L   |
| 586 | TAC | CAA | CAG | AAA | CCA | GGA | CAG | CCA | CCC | AAA | CTC | CTC | ATC | TAT | CTT |
|     | ATG | GTT | GTC | TTT | GGT | CCT | GTC | GGT | GGG | TTT | GAG | GAG | TAG | ATA | GAA |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| +1  | A   | S   | N   | L   | E   | S   | G   | V   | P   | A   | R   | F   | S   | G   | S   |
| 631 | GCA | TCC | AAC | CTA | GAA | TCT | GGG | GTC | CCT | GCC | AGG | TTC | AGT | GGC | AGT |
|     | CGT | AGG | TTG | GAT | CTT | AGA | CCC | CAG | GGA | CGG | TCC | AAG | TCA | CCG | TCA |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| +1  | G   | S   | G   | T   | D   | F   | T   | L   | N   | I   | H   | P   | V   | E   | E   |
| 676 | GGG | TCT | GGG | ACA | GAC | TTC | ACC | CTC | AAC | ATC | CAT | CCT | GTG | GAG | GAG |
|     | CCC | AGA | CCC | TGT | CTG | AAG | TGG | GAG | TTG | TAG | GTA | GGA | CAC | CTC | CTC |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| +1  | E   | D   | A   | A   | T   | Y   | Y   | C   | Q   | H   | S   | R   | E   | L   | P   |
| 721 | GAG | GAT | GCT | GCA | ACC | TAT | TAC | TGT | CAG | CAC | AGT | AGG | GAG | CTT | CCT |
|     | CTC | CTA | CGA | CGT | TGG | ATA | ATG | ACA | GTC | GTG | TCA | TCC | CTC | GAA | GGA |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |        |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|
| +1  | R   | T   | F   | G   | G   | G   | T   | K   | L   | E   | I   | K   | R   | Spacer |     |
| 766 | CGG | ACG | TTC | GGT | GGA | GGC | ACC | AAG | CTG | GAA | ATC | AAA | CGG | A      | A   |
|     | GCC | TGC | AAG | CCA | CCT | CCG | TGG | TTC | GAC | CTT | TAG | TTT | GCC | GCG    | GCC |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | CGC    | CGG |

|     |     |         |     |     |     |     |     |     |     |     |     |     |     |        |     |
|-----|-----|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|
|     |     | Myc-tag |     |     |     |     |     |     |     |     |     |     |     | Spacer |     |
| +1  | A   | E       | Q   | K   | L   | I   | S   | E   | E   | D   | L   | N   | G   | A      | A   |
| 811 | GCA | GAA     | CAA | AAA | CTC | ATC | TCA | GAA | GAG | GAT | CTG | AAT | GGG | GCG    | GCA |
|     | CGT | CTT     | GTT | TTT | GAG | TAG | AGT | CTT | CTC | CTA | GAC | TTA | CCC | CGC    | CGT |

|     |         |     |     |     |     |     |     |
|-----|---------|-----|-----|-----|-----|-----|-----|
|     | His tag |     |     |     |     |     |     |
| +1  | H       | H   | H   | H   | H   | H   | *   |
| 856 | CAT     | CAC | CAT | CAC | CAT | CAC | TAA |
|     | GTA     | GTG | GTA | GTG | GTA | GTG | ATT |

Fig. 35-2



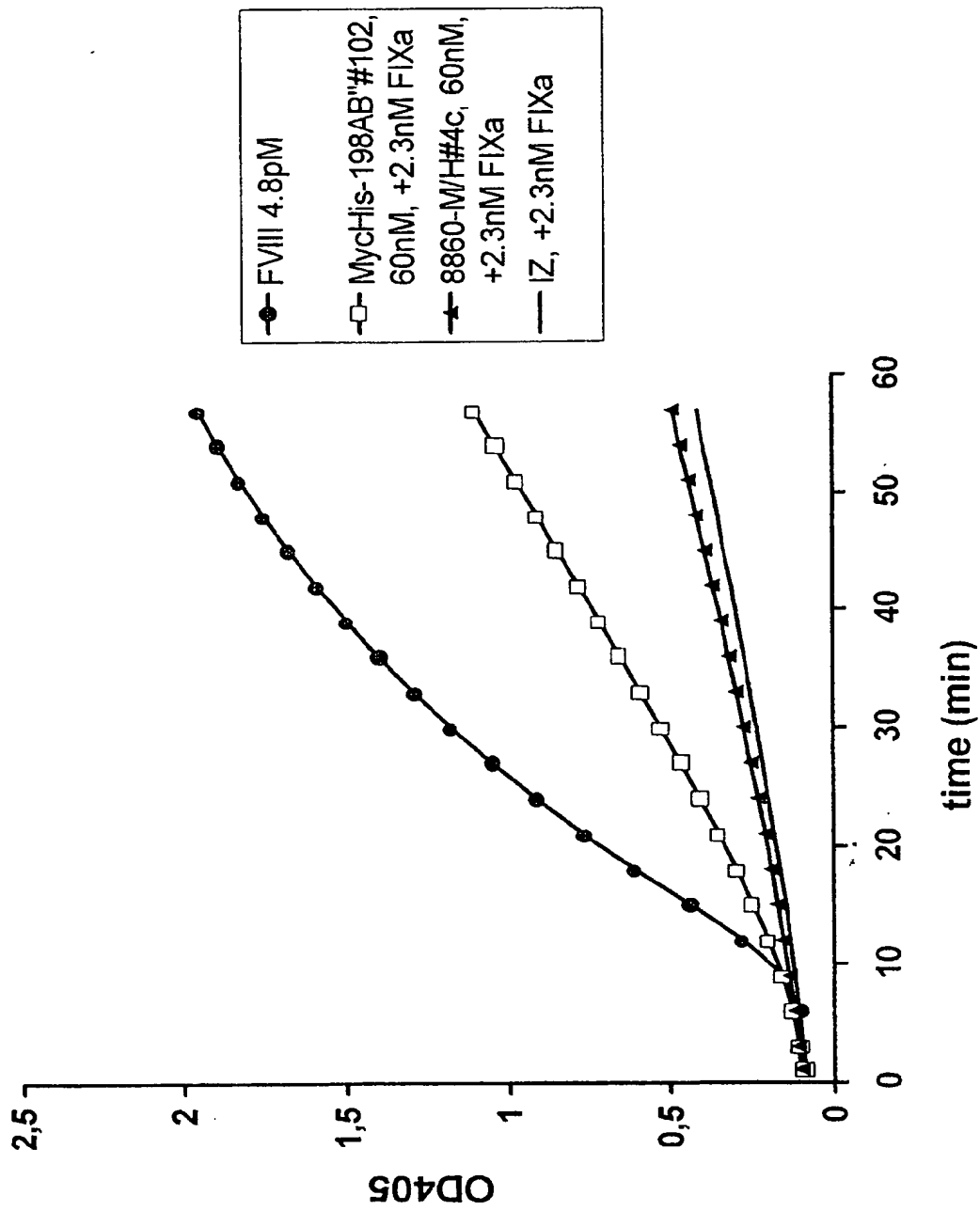


Fig. 36

## REFERENCES CITED IN THE DESCRIPTION

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